



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 181983

TO: Robert M Kelly
Location: rem/2C55/2C70
Art Unit: 1633
Friday, March 17, 2006
Case Serial Number: 10/811028

From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Examiner Kelly,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port
X22523

This Page Blank (uspto)

STIC-Biotech/ChemLib

181983

mg

From: Kelly, Robert
Sent: Saturday, March 11, 2006 9:22 AM
To: STIC-Biotech/ChemLib
Subject: 10/811,028

RECEIVED
MAR 13 2006
(S16)

Please search:

SEQ ID NO: 1

Robert M. Kelly, Ph.D.
Art Unit 1633
Room 2C55, Remsen Bldg.
Mailbox 2C70
(571) 272-0729

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

This Page Blank (usp10)

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1937	44.7	3609	6	AX249944	Sequence
2	1924.4	44.4	3589	6	AX249943	Sequence
3	1923.8	44.4	3589	6	BD136051	Interfero
4	1845.4	42.6	8349	6	BD260598	Sequence
5	1836.8	42.4	2661	11	SYNRKMRG	
6	1821.8	42.1	2999	11	SYNCCDDB	
7	1821.8	42.1	2999	11	SYNCCDDB	
8	1817.8	42.0	2959	11	AF402779	Expressio
9	1780.8	41.1	2604	11	AY189826	His-3 int
10	1780.8	41.1	11373	11	AY189827	His-3 int
11	1780.8	41.1	11403	11	AY189829	His-3 int
12	1719	39.7	3600	6	BD063789	Insulin-1
13	1719	39.7	3600	6	BD063040	treatment
14	1718.4	39.7	3426	6	BD136049	Interfero
15	1718.4	39.7	3534	6	CQ854723	Sequence
16	1718.4	39.7	3534	6	CQ854724	Sequence
17	1718.4	39.7	3534	6	CQ854725	Sequence
18	1718.4	39.7	3534	6	CQ854726	Sequence

QY 381 GACGTCATTAATGAGTATGTTCCATAGTAAGCCCAATAGGACTTTCCATTGACGTCA 440
 DB |||||
 QY 86 GACGTCATTAATGAGTATGTTCCATAGTAAGCCCAATAGGACTTTCCATTGACGTCA 145
 DB |||||
 QY 441 ATGGGTGGAGTATTTACGGTAACTGCCATCTGGCAGTACATCAAGTGTATCATATGCC 500
 DB |||||
 QY 146 ATGGGTGGAGTATTTACGGTAACTGCCATCTGGCAGTACATCAAGTGTATCATATGCC 205
 DB |||||
 QY 501 AAGTACGCCCTTATGACGTCATGACGGTAAATGGCCCGCTGGCAATATGCCAGTA 560
 DB |||||
 QY 206 AAGTACGCCCTTATGACGTCATGACGGTAAATGGCCCGCTGGCAATATGCCAGTA 265
 DB |||||
 QY 561 CATGACCTTATGGGACTTTCTTACTTGGCAGTACATCTACGATATAGTCAFCGTATPAC 620
 DB |||||
 QY 266 CATGACCTTATGGGACTTTCTTACTTGGCAGTACATCTACGATATAGTCAFCGTATPAC 325
 DB |||||
 QY 621 CATGGTGAATGGGTTTGGGAGTACATCAATGGGGGTGGATAGCGGTTTGACTCACGGGG 680
 DB |||||
 QY 326 CATGGTGAATGGGTTTGGGAGTACATCAATGGGGGTGGATAGCGGTTTGACTCACGGGG 385
 DB |||||
 QY 681 ATTTCCAGTCTCCACCCCATTTGACGTCATGAGGTTTGTGGTGGCACCACCAATCAACG 740
 DB |||||
 QY 386 ATTTCCAGTCTCCACCCCATTTGACGTCATGAGGTTTGTGGTGGCACCACCAATCAACG 445
 DB |||||
 QY 741 GGACTTTCCAAAATGTCGTAAACCTCCGCCCATTTGACGCAAAATGGCGGTAGCGGTGT 800
 DB |||||
 QY 446 GGACTTTCCAAAATGTCGTAAACCTCCGCCCATTTGACGCAAAATGGCGGTAGCGGTGT 505
 DB |||||
 QY 801 ACGTGGGAGTCTATATAGCAGAGCTCGTTTGTAGTGAACGTCAGATCGCTCGGAGACG 860
 DB |||||
 QY 506 ACGTGGGAGTCTATATAGCAGAGCTCGTTTGTAGTGAACGTCAGATCGCTCGGAGACG 565
 DB |||||
 QY 861 CCATCCAGCTGTTTGTGACCTCCATAGAAAGACACCGGACCGATCCAGCTGACTCTAGC 920
 DB |||||
 QY 566 CCATCCAGCTGTTTGTGACCTCCATAGAAAGACACCGGACCGATCCAGCTCGGCGCGG 625
 DB |||||
 QY 921 CTAGCTCTGAAGTGGTGGTGGAGCCCTGGGACAGGTTGGTATCAAGGTTTCAAGACAGGT 980
 DB |||||
 QY 626 GNAACGGTGCAATGGAAACGCG----- 646
 DB |||||
 QY 981 TTAGGAGACCAATAGAAACTGGGCATGTGGAGACAGAGACACTCTTGGGTTCTGTATA 1040
 DB |||||
 QY 647 -----GATTCCCGGTGTTAAATTAACAGGTAAGTGCTTCCCTCGTGTTC 691
 DB |||||
 QY 1041 GGCAGTGACTCTCTGCTCTATGCTATTTTCCACCTTAGGCTGTGCTGCTAGCC 1100
 DB |||||
 QY 692 TTCCCTCGTATCTGCTCAACTTCCATCAGAACTGCAGTATCTGTATTTTGTCTAG 751
 DB |||||
 QY 1101 TAGGAGATCTCTCGAGGTGACGGTATCGATAGAGCTTGAATTCGGGGCGGCGGA 1160
 DB |||||
 QY 752 CAGTAATACTAACGGTCTCTTTTCTCTTCAAGGCCACCAAGCTTCCATGGGGGTGCC 811
 DB |||||
 QY 1161 GGAGCGGCACTCGTGGCTGTGGCTTCGGCAGCGGCTTCAGAGATCGCGGCATCAG 1220
 DB |||||
 QY 812 CGAACGCCCCACCTGCTGCTCTCTCTCTCTGCTGATTCCTCTGGGCTCCAGT 871
 DB |||||
 QY 1221 CGGTAGCACACGACTAGCAGCATGTTGACCGCGGCGAGTGTGCGGCACACGAGGAGCT 1280
 DB |||||
 QY 872 CTTCTGTGCTCCGCCACGCTCATCTGCGACAGTCCGGTGTGGAGAGGTACATCCTGGA 931
 DB |||||
 QY 1281 GGCCTCGGTTTTGGGTATCTGGGCTTCAGGAGAGACACAGCTCCCGCCTTCCGCTTA 1340
 DB |||||
 QY 932 GGCCAAGG-----AGGCAGAAAATGTCAAGTGGGTTGTGAGAA 971
 DB |||||
 QY 1341 CGACTACGCGGCCCTGGAACTTCAATCAACGCGCAGATCATGCGAGTGCACACAGCAA 1400
 DB |||||
 QY 972 GGTCCACAGACTGAGTGA-- 990
 DB |||||
 QY 1401 GCACCAACGCGGCTTACGTGAACCACTGAACTGACCGAGGAGAGTACAGAGGCGGTT 1460
 DB |||||
 QY 991 --ATATTACAGTCCCAGATACCAAAAGTCAACTTCTATGCTTGGAAAAGAAATGAGGTGA 1048
 DB |||||

QY 1461 GGCCAGGGAGATGTTACAGCCCATAGTCTTTCAGCCTGCACCTGAAGTTCAATGGTGG 1520
 DB |||||
 QY 1049 AGAACAGG-----CCATCGAAGTGTGGCAAGCCCTGTCCCTGCTCAGCGAAGCCATCCTGC 1104
 DB |||||
 QY 1521 TGGTCATATCAATCATAGCATTTTCTGGACAAACCTCAGCCCTAACCGTGTGGAGAAC 1580
 DB |||||
 QY 1105 AGGCCAGGCGCTGCTGGCCAAATTCCTCCAGCCACCCAGAGACCTGCGAGTGCATATCG 1164
 DB |||||
 QY 1581 CAAAGGGAGGTGCTGGAAGCCATCAAAACGTGAATTTGGTTCCTTTGACAAAGTTTAAAG 1640
 DB |||||
 QY 1165 ACAAAGCCATCAGTGTCTGC----- 1185
 DB |||||
 QY 1641 GAAGCTACGGCTGCATCTGTTGGTGTCCAAGGCTCAGGTTGGGTTGGCTTGGTTTCAA 1700
 DB |||||
 QY 1186 -----GCAGCTCACTTCCCTGCTGCGGGTCTCGGAGCTCAG 1223
 DB |||||
 QY 1701 TAAGGAACGGGACACATTACAAATTTGCTGTTCCTTCCAAATCAGGATCCACTGCAAGGAAC 1760
 DB |||||
 QY 1224 AAGGAATGTATGTCCTCCCTCCAGAT----- 1247
 DB |||||
 QY 1761 AACAGGCTTTATCCACTGCTGGGGATGATGTGTGGAGACACGTTTACTTACTTCACTA 1820
 DB |||||
 QY 1248 -----ACCAACCCCACTGCTCCACTCC 1269
 DB |||||
 QY 1821 TAAAAATGTGAGGCTGATTTATCTAAAGCTATTTTGGAACTGAATCACTCACTGGGAGATG 1880
 DB |||||
 QY 1270 GCACACTCACAGTGGATCTTTCTGCAAGCTCTTCCGGGTCTACGCCA----- 1317
 DB |||||
 QY 1881 TAAGTAAAGATACATGCTTTCGCAAAAGTAAACCAACGATCGTTTATGCTGGAAAAA 1940
 DB |||||
 QY 1318 -----ACTTCTCCGGGGAACTGAAGCTGTACACGGGAGAGGTCTG 1360
 DB |||||
 QY 1941 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 2000
 DB |||||
 QY 1361 CAGGAGAGGGACAGGTGAGTC-----TAGAAAAGCCGAAATTTCTGCAGG 1404
 DB |||||
 QY 2001 GCCCGGGGATCCACTAGTTCTTAGAGCGCGCCACCGCGTGGAGCTCCCAACTAGAA 2060
 DB |||||
 QY 1405 AATTGGGTGGCATCCCTGTGACCCCTCCCAAGTGCCTCTCTGGGCCCTGGAAAGTTGCCAC 1464
 DB |||||
 QY 2061 TGCAGTGAATAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAAACA 2120
 DB |||||
 QY 1465 TCCAGTGGCCACCAGGCTTGTCTTAATAAATTAAGTTGCATCAATTTGTCTGACTAGT 1524
 DB |||||
 QY 2121 TTATAAGCTGCATTAACAAAGTTAAACAATTCATTTATGTTTATGTTTTCAGGTTTCAGG 2180
 DB |||||
 QY 1525 GTCTTCTTAATAATTTATGGGGTGGAGGGGGTGGTATGGAGCAAGGGGCAAGTTGGGAA 1584
 DB |||||
 QY 2181 GGGAGGTGTGGAGGTTTTTTTAAAGCCACAGCTCCAGCTTTTGTTCCTTTTGTAGTGAGGT 2240
 DB |||||
 QY 1585 GACAACCTGTAGGGCTCGAGGGGGGGCCGGTACCAGCTTTTGTTCCTTTTGTAGTGAGGT 1644
 DB |||||
 QY 2241 TAAATTCAGGCTTGGCGTAATCAGGTCATAGCTGTTTCTGTGTGAAATTTGTATTCGCG 2300
 DB |||||
 QY 1645 TAAATTCAGGCTTGGCGTAATCAGGTCATAGCTGTTTCTGTGTGAAATTTGTATTCGCG 1704
 DB |||||
 QY 2301 TCACAAATTCACACAACTACAGCGGAGCAATAGTGTAAAGCTTGGGTTGGCTTAT 2360
 DB |||||
 QY 1705 TCACAAATTCACACAACTACAGCGGAGCAATAGTGTAAAGCTTGGGTTGGCTTAT 1764
 DB |||||
 QY 2361 GAGTCAGCTTAACATCACTTAATTTGCTTGCCTCACTGCCCTTTTCCAGTGGGAAAC 2420
 DB |||||
 QY 1765 GAGTCAGCTTAACATCACTTAATTTGCTTGCCTCACTGCCCTTTTCCAGTGGGAAAC 1824
 DB |||||
 QY 2421 TGTCTGTCAGCTGCTAATTAATCGGCAACCGCGGGGAGAGCGGTTTTCGCTATTG 2480
 DB |||||
 QY 1825 TGTCTGTCAGCTGCTAATTAATCGGCAACCGCGGGGAGAGCGGTTTTCGCTATTG 1884
 DB |||||
 QY 2481 GCGGCTTCTCCGCTTCCCTCACTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 2540
 DB |||||
 QY 1885 GCGGCTTCTCCGCTTCCCTCACTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 1944
 DB |||||
 QY 2541 CGGTATCAGCTCACTCAAAAGGCGGTAATACGGTTATTCACAGAAATCAGGGATTAACGCAG 2600
 DB |||||

1945 CCGTATCAGCTCACTCAAGGCGGTAAATACGTTTATCCACAGATCAGGGGATAACCGAG 2004
 2601 GAAAGACATGTGAGCAAAAGGCGCAGCAAAAGGCGAGAACCGTAAAGAGCGCGGTTC 2660
 2005 GAAAGACATGTGAGCAAAAGGCGCAGCAAAAGGCGAGAACCGTAAAGAGCGCGGTTC 2064
 2661 TGGCGTTTTCATAGGCTCGCGCCCTCTGACGAGCATCAAAAATCGAGCTCAAGTC 2720
 2065 TGGCGTTTTCATAGGCTCGCGCCCTCTGACGAGCATCAAAAATCGAGCTCAAGTC 2124
 2721 AGAGTGCGCAAAACCGACAGGACTATAAGATACAGAGGCTTTCCCTCTGAAAGCTCCC 2780
 2125 AGAGTGCGCAAAACCGACAGGACTATAAGATACAGAGGCTTTCCCTCTGAAAGCTCCC 2184
 2781 TCGTGCCTCTCTCTGTTCCGACCTCGCGCTTACCGGATACCTGTCCGCTTCTCCCTT 2840
 2185 TCGTGCCTCTCTCTGTTCCGACCTCGCGCTTACCGGATACCTGTCCGCTTCTCCCTT 2244
 2841 CGGGAAGCGTGGCGCTTTCTCAATGCTCAGCTGTAGGTATCTCAGTTCCGTTGAGGTGC 2900
 2245 CGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCGTTGAGGTGC 2304
 2901 TTGCTCCAAGCTGGCTGTGTGCAAGAACCCCTCGTTCAAGCCGCGAGCTGGCGCTTAT 2960
 2305 TTGCTCCAAGCTGGCTGTGTGCAAGAACCCCTCGTTCAAGCCGCGAGCTGGCGCTTAT 2364
 2961 CCGGTAATCTCGTCTTGTAGTCCAAACCGGTAGACACGACTTATCCCACTGGCAGCAG 3020
 2365 CCGGTAATCTCGTCTTGTAGTCCAAACCGGTAGACACGACTTATCCCACTGGCAGCAG 2424
 3021 CCATGTTAAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGTGTACAGAGTTCTTGAAGT 3080
 2425 CCATGTTAAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGTGTACAGAGTTCTTGAAGT 2484
 3081 GGTGGCTTAAGTCTAGCTTACACTAGAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGC 3140
 2485 GGTGGCTTAAGTCTAGCTTACACTAGAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGC 2544
 3141 CAGTTACTCTCGGAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACACCGCTGGTA 3200
 2545 CAGTTACTCTCGGAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACACCGCTGGTA 2604
 3201 CGCGTGGTTTTTTTGTGCAAGCAGCAGATTAGCGCAGAAAAAGGATCTCAAGAAG 3260
 2605 CGCGTGGTTTTTTTGTGCAAGCAGCAGATTAGCGCAGAAAAAGGATCTCAAGAAG 2664
 3261 ATCCTTTGATCTTTCTACGGGTCTGACGCTCAGTGGAAACGAAACTCAGTTAAGGGA 3320
 2665 ATCCTTTGATCTTTCTACGGGTCTGACGCTCAGTGGAAACGAAACTCAGTTAAGGGA 2695
 3321 TTTTGGTCAATGAGCGGATACATATTTGAAATGATTTTGAAGAAATAAACAATAGGGGTT 3380
 2696 ----- 2695
 3381 CGCGCACATTTCCCGAAAAAGTGCCACCTGTATGCGGTGTGAAATACCGCACAGATCGT 3440
 2696 ----- 2695
 3441 AAGGAGAAATACCGCATCAGGAAATGTAAGCGTTAATTAATTCAGAGAACTCGTCAAG 3500
 2696 -----TCAGAGAACTCGTCAAG 2713
 3501 AAGCGGATAGAAGCGATGCGTCCGAATCGGAGCGCGGATACCGTAAAGACGAGGAA 3560
 2714 AAGCGGATAGAAGCGATGCGTCCGAATCGGAGCGCGGATACCGTAAAGACGAGGAA 2773
 3561 CGCGTACGCCATTCGCGCCCAAGCTCTTCAGCAATATCAGGATACCGGATACCGGATATGC 3620
 2774 CGCGTACGCCATTCGCGCCCAAGCTCTTCAGCAATATCAGGATACCGGATACCGGATATGC 2833
 3621 CTGATAGCGTCCGCGCACCCAGCGGCGCACAGTGTGATGAATCCAGAAAGCGGCATT 3680

2834 CTGATAGCGTCCGCGCACACCCAGCGGCGCACAGTCGATGATGATCCAGAAAGCGGCCATT 2893
 3681 TTCCACCATCATATTTCGGCAAGCAGGCATCGCCATGSGGTCAAGCAGAGATCTTCGCCGTC 3740
 2894 TTCCACCATCATATTTCGGCAAGCAGGCATCGCCATGCGTCAAGCAGAGATCTTCGCCGTC 2953
 3741 GGGCATGCTCGCTTCAGCTTCGAGCTTCGAGTTCGCGTGGCGGAGCCCTGATGCTCTTC 3800
 2954 GGGCATGCGCGCTTCAGCTTCGAGTTCGAGTTCGCGTGGCGGAGCCCTGATGCTCTTC 3013
 3801 GTCAGATCATCTGATTCGACAAAGACCGGCTTCATCCGAGTACGTCGCTCGATGCG 3860
 3014 GTCAGATCATCTGATTCGACAAAGACCGGCTTCATCCGAGTACGTCGCTCGATGCG 3073
 3861 ATGTTTCGCTTCGTTGCTGGAATCGGAGTTCGCGGATCAAGGATGTCAGCGCGCCAT 3920
 3074 ATGTTTCGCTTCGTTGCTGGAATCGGAGTTCGCGGATCAAGGATGTCAGCGCGCCAT 3133
 3921 TGCATCAGCCATCATGATGATATCTTCTCGGAGGAGCAAGGTGAGATGACAGGAGATCTG 3980
 3134 TGCATCAGCCATCATGATGATATCTTCTCGGAGGAGCAAGGTGAGATGACAGGAGATCTG 3193
 3981 CCCCGGCACTTCGCCCAATAGCAGCAGTCCCTTCGCGTTTCAGTGAACAGCTGAGCAG 4040
 3194 CCCCGGCACTTCGCCCAATAGCAGCAGTCCCTTCGCGTTTCAGTGAACAGCTGAGCAG 3253
 4041 AGCTGCGCAGGAAACCGCGTTCGTCGCGCAGCAGTACGCGCTGCTGCTCTTCGAG 4100
 3254 AGCTGCGCAGGAAACCGCGTTCGTCGCGCAGCAGTACGCGCTGCTGCTCTTCGAG 3313
 4101 TTCAATTCAGGCAACCGGACAGGTCGCTTTGACAAAGAAACCGGCGCGCTTCGCTGTA 4160
 3314 TTCAATTCAGGCAACCGGACAGGTCGCTTTGACAAAGAAACCGGCGCGCTTCGCTGTA 3373
 4161 CAGCGGACACCGCGGATCAGAGCAGCGATGCTGTGTGTCGCGCAGTATAGCCGAA 4220
 3374 CAGCGGACACCGCGGATCAGAGCAGCGATGCTGTGTGTCGCGCAGTATAGCCGAA 3433
 4221 TAGCCTCTCCACCAAGCGCGGAGAACCTGCGTCAATCCATCTTTGTTCAATCATGCG 4280
 3434 TAGCCTCTCCACCAAGCGCGGAGAACCTGCGTCAATCCATCTTTGTTCAATCATGCG 3493
 4281 AAACGATCTCTCATCTCTCTCTTGTATCAGAGCTTGTATCCCTCGCGCCATCAG 4332
 3494 AAACGATCTCTCATCTCTCTCTTGTATCAGATCTTGTATCCCTCGCGCCATCAG 3545

RESULT 2
 AX249943
 LOCUS 3589 bp DNA linear PAT 28-SEP-2001
 DEFINITION Sequence 1 from Patent WO0166149.
 ACCESSION AX249943
 VERSION AX249943.1 GI:15864429
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Fewell,J.G., MacLaughlin,F., Smith,L.C., Nicol,F. and Rolland,A.
 TITLE Nucleic acid formulations for gene delivery and methods of use
 JOURNAL Patent: WO 0166149-A 1 13-SEP-2001;
 Valentis, Inc. (US)
 FEATURES
 Location/Qualifiers
 1..3589
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Expression plasmid pIF0921 encoding for human
 interferon alpha (7 68) --- (1334)."
 768..1334
 /note="unnamed protein product"
 /codon_start=1
 /transl_table=1

/protein_id="CAC88666.1"
/db_xref="GI:15864430"
/translation="MALTFALLVLLSKSSVSGCDLPOTHSLGSRRTLLMLAOM
RRISLFSCLKNRHDGFPQBEFGNFOKAEIPIVLHEMIQIENLFSTKDSAAWDET
LLDKFYTELQQLNDLEACVUIQGVGTETPLMKEDSLAVRKYPQRIPLYLKEKYSP
CAWEVRAEIMRISFSLSTNLQESLRSKE"

ORIGIN

Query Match 44.4%; Score 1924.4; DB 6; Length 3589;
Best Local Similarity 72.1%; Pred. No. 0;
Matches 2892; Conservative 0; Mismatches 607; Indels 514; Gaps 9;
Qy 321 CGTTACATAACTACGTAATAATGCGCCCTGGCTGACCGGCCAACGACCCCGCCCAATT 380
Db 1 CGTTACATAACTACGTAATAATGCGCCCTGGCTGACCGGCCAACGACCCCGCCCAATT 60
Qy 381 GACGTCATATGACGTATGTTCCCATAGTAACGCCAATAGGAGCTTTCCATTGACGTCA 440
Db 61 GACGTCATATGACGTATGTTCCCATAGTAACGCCAATAGGAGCTTTCCATTGACGTCA 120
Qy 441 ATGGGTGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCC 500
Db 121 ATGGGTGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCC 180
Qy 501 AAGTACGCCCTATATGACGTCAATGACGTAATGACGTAATGACGTAATGACGTAATGACGTA 560
Db 181 AAGTACGCCCTATATGACGTCAATGACGTAATGACGTAATGACGTAATGACGTAATGACGTA 240
Qy 561 CATGACCTTATGGGATTTCTGCTGACGTACATCTACGTATGATGATGATGATGATGATGATGAT 620
Db 241 CATGACCTTATGGGATTTCTGCTGACGTACATCTACGTATGATGATGATGATGATGATGATGAT 300
Qy 621 CATGCTGATGGGTTTGGCAGTACATCAATGGCGCTGGATAGCGGTTGACTCAACGGGG 680
Db 301 CATGCTGATGGGTTTGGCAGTACATCAATGGCGCTGGATAGCGGTTGACTCAACGGGG 360
Qy 681 ATTTCCAAAGTCTCCACCCCAATGACGTAATGACGTAATGACGTAATGACGTAATGACGTAATGACG 740
Db 361 ATTTCCAAAGTCTCCACCCCAATGACGTAATGACGTAATGACGTAATGACGTAATGACGTAATGACG 420
Qy 741 GGACTTTCCAAATCTGCTGACAACTCCGCCCATTTGACGCAAAATGGCGGTAGCGGTGT 800
Db 421 GGACTTTCCAAATCTGCTGACAACTCCGCCCATTTGACGCAAAATGGCGGTAGCGGTGT 480
Qy 801 ACGGTGGAGGTCTATATAAGCAGAGCTGCTTTAGTGAAACGCTCAGATGCGCTGGAGACG 860
Db 481 ACGGTGGAGGTCTATATAAGCAGAGCTGCTTTAGTGAAACGCTCAGATGCGCTGGAGACG 540
Qy 861 CCATCAGCGCTGTTTGAACCTCCTAGAGACACCGGACCGATCCAGCTGACTCTAGC 920
Db 541 CCATCAGCGCTGTTTGAACCTCCTAGAGACACCGGACCGATCCAGCTCCTCGCGGCGG 600
Qy 921 CTAGCTCTGAAGTGTGGTGGAGGCCCTGGCGAGGTTGGTATCAAGGTTTACAAGACAGGT 980
Db 601 GGAAAGGTCATGGNACG----- 619
Qy 981 TTAAGGAGACCAATAGAAACTGGGCATGTGGAGACAGAGAGACTTTGGGTTTCTGATA 1040
Db 620 -----CGGATTCCTCCGT 631
Qy 1041 GGCACGTGACTCTCTGCGCTATTTGGTCTATTTTCCACCCCTTAGGCTGCTGCTGAGCC 1100
Db 632 GTTAATTAAAGAGTAAGTGTCTTCTGCTGTTTCTTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 685
Qy 1101 TAGGAGATCTCTCGAGGTGCAAGGTATCGATAGCTTGTATCGAATTCCTGGGCGCGCA 1160
Db 686 ----- 685
Qy 1161 GGAGCGGCACTCGTGGCTGTGGTGGCTTGGCGAGCGGCTTACGACAGATCGGCGGCATCAG 1220
Db 686 -----AACCTTCTTATCAGAAACTGCAG 708
Qy 1221 CGGTAGCACCGACCTAGCAGCATGTTGAGCGGGCAGTGTGGCGCACCGACGAGGCAGC- 1279

Db 709 TATCTGTATTTTGTAGCAGTAATACTAAACGGTCTCTTTTCTTCTTCTCAGGCCACCA 768
Qy 1280 TGGTCTCCGGTTTTGGGGTATCTGGGGTCTCAGGCGAAGACACAGCTCCCGACCTGCCCT 1339
Db 769 TGGCTTGACCTTGTCTTACTGGTGGCCCTCTCTGGTGTCTCAGC-----TGCAAGTCA 821
Qy 1340 ACGACTACGGCGCCCTGGAAACCTCACAATCAACGGCGAGATCATGACGCTGCACACAGCA 1399
Db 822 AGCTGCTCTGTGGGCTGTGATCTGCCTCAAAACCCACAGCTGGGTAGCAGGAGACCTTG 881
Qy 1400 AGCACCAACGGCGCTAGTGAACCAACCTGAAACGTCAACGAGGAGAACTACCAAGGCGCT 1459
Db 882 ATGCTCTCTGGCAGATGAGGAGATCTCTCTTTCTCTCTGCTTGAAGACAGACAG----- 935
Qy 1460 TGGCAAGGAGAGATGTTACAGCCAGATAGCTCTTACGCCCTGCACTGAAGTTCATGCTG 1519
Db 936 -----CATGACTTTGGATTTCCCGCAGGAGGAGTTTGGCAACCACTTCCAAAGGCTGAAA 990
Qy 1520 GTGGTCATATCAATCATAGCATTTTCTGGCAAAACCTCAGCCCTAAACGGTGGTGGAGAAC 1579
Db 991 CCATCCCTGTCTCCATGAGATGATCCAGCAGATCTTCAATCTCTTACGACAAGGACT 1050
Qy 1580 CCAAGGCGGAGTTCTGGAAGCCATCAAACTGACTTTTGGTCTCTTTGACAAAGTTTAAAG 1639
Db 1051 CATCTGCTGTTGGATGAGACCTCTCTAGACAAATTTCTACACTGAACTCTACACGACAG 1110
Qy 1640 AGAAGCTGACCGCTGCACTGTTGGTGTCAAGGCTCAGGTTGGGTTGGCTTGGTTTCA 1699
Db 1111 TGAATGACCTTGAAGCCTGTGT-----GATACAGGGGGTGGGGGTGACAGAGACTCCC 1163
Qy 1700 ATAGGAAACGGGGACACTTACAAATGCTGCTGTCGTAATCAGGATCCACTGCAAGNA 1759
Db 1164 CTGATGAAGGAGGACTC----- 1180
Qy 1760 CAACAGGCTTATTTCCACTGCTGGGATTTGATGTGTGGGAGACGCTTACTACTTCACT 1819
Db 1181 -----CATTTCTGGCTGTGAGGAATACTTCCAAAGAAATCACTCTCTATCTGAAAG 1230
Qy 1820 ATAAAAATGTGAGGCTGATTTATCTAAAGCTATTTGGAATGTAACTGAGGAGAGAT 1879
Db 1231 AGAAGAAATACAGCCCTTGTCTGGGAGGTTGTGACAGCAGAAATCATGAGATCTTTT 1290
Qy 1880 GTAACCTGAAAGATACATGCTTGGCAAAAGTAAACACGATCGTTATGCTGGAAGAAAA 1939
Db 1291 CTTTGTCT----- 1298
Qy 1940 AAAGGAAATCCCTGC 1999
Db 1299 ACNAACTTGCAGAAAGTTTAAAGATTAAGGAATGAATCTAGAAAGCGGAATTTGCGAG 1358
Qy 2000 AGCCCGGGGATTCATAGTCTAGAGCGCGCCACCGCGGTGAGCTCCCAACTAGA 2059
Db 1359 GAAATGGGTGGCATCCCTGTGACCCCTCCAGTGCCTCTCCTGCGCCCTGGAAAGTTGCCA 1418
Qy 2060 ATGCAAGTGAAGAAATGCTTTATTTGTGAATTTGTGATGCTATTTGCTTTTGTAAACC 2119
Db 1419 CTCCAGTGCCCAACAGCTTGTCTTAATAAATTAAGTTGCAATCATTTTGTCTGACTAGG 1478
Qy 2120 ATTATAAGCTGCAATAAACAAGTTTAAACAACAATTCATTTTATGTTTTCAGTTTCAG 2179
Db 1479 TGTCTCTTCTATATATTTATGGGGTGGAGGGGGTGGTATGGAGCAAGGGCAAGTTGGGA 1538
Qy 2180 GGGGAGGTGGGAGGTTTTTAAAGCCACAGCTCCAGCTTTTGTTCCTTTTGTAGTGAGG 2239
Db 1539 AGACAACCTGTATGGGCTCGAGGGGGGGCCGGTACAGCTTTTGTTCCTTTTGTAGTGGG 1598
Qy 2240 TTAATTTTCAGCTTGGCGTAATCATGCTCATAGCTGTTTCTCTGTGTAATTTTATCCG 2299
Db 1599 TTAATTTTCAGCTTGGCGTAATCATGCTCATAGCTGTTTCTCTGTGTAATTTTATCCG 1658
Qy 2300 CTCACAATTTCCACAACAATACGAGCCGGAGACATTAAGCTTAAAGCTTGGGTGCTTAA 2359

Db 1659 CTCAAAATCCACAACAATACGACGCGGAAGCATAAAGTGTAAAGCTCGGGGTGCCTAA 1718
Qy TGAGTGAAGCTAACTCACATTAATTCGCTGCGCTCACTGCGCGCTTCCAGTTCGGGAAC 2419
Db 1719 TGAGTGAAGCTAACTCACATTAATTCGCTGCGCTCACTGCGCGCTTCCAGTTCGGGAAC 1778
Qy 2420 CTGTCGTGCGAGCTGCAATTAATGAATCGGCCAACCGCGGGGAGAGCGGTTCGCTGATT 2479
Db 1779 CTGTCGTGCGAGCTGCAATTAATGAATCGGCCAACCGCGGGGAGAGCGGTTCGCTGATT 1838
Qy 2480 GGGCGCTCTTCGCTCTCTGCTCACTGATCTGCTGCGCTCGCTGCTGCTGCGCGGA 2539
Db 1839 GGGCGCTCTTCGCTCTCTGCTCACTGATCTGCTGCGCTCGCTGCTGCTGCGCGGA 1898
Qy 2540 GCGGTATCAGCTCACTCAAGAGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACGCA 2599
Db 1899 GCGGTATCAGCTCACTCAAGAGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACGCA 1958
Qy 2600 GGAAGAAATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAAGAGCGCGTTG 2659
Db 1959 GGAAGAAATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAAGAGCGCGTTG 2018
Qy 2660 CTGCGCTTTTCCATAGGCTCCGCGCTGAGAGGCTTAAAGATACCAAGGCTCAAGT 2719
Db 2019 CTGCGCTTTTCCATAGGCTCCGCGCTGAGAGGCTTAAAGATACCAAGGCTCAAGT 2078
Qy 2720 CAGAGTGGGGAACCCGACAGGACTATAAGATACCAAGGCTTTCCCGCTGGAAGCTCC 2779
Db 2079 CAGAGTGGGGAACCCGACAGGACTATAAGATACCAAGGCTTTCCCGCTGGAAGCTCC 2138
Qy 2780 CTCGTGCGCTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCGCGCTTTCTCCCT 2839
Db 2139 CTCGTGCGCTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCGCGCTTTCTCCCT 2198
Qy 2840 TCGGGAAGCTGGCGCTTCTCAATGCTCAGCTGAGTATCTCAGTTCGCTGAGTGC 2899
Db 2199 TCGGGAAGCTGGCGCTTCTCATAGCTCAGCTGAGTATCTCAGTTCGCTGAGTGC 2258
Qy 2900 GTTCGCTCCAGCTGGGCTGTGTGACAGAACCCCGCTTCAGCGCCGACCGCTGCGCTTA 2959
Db 2259 GTTCGCTCCAGCTGGGCTGTGTGACAGAACCCCGCTTCAGCGCCGACCGCTGCGCTTA 2318
Qy 2960 TCGGTAATCTATGCTTTGAGTCAACCCGGTAAGACACGACTTATCGCCACTGGGACGA 3019
Db 2319 TCGGTAATCTATGCTTTGAGTCAACCCGGTAAGACACGACTTATCGCCACTGGGACGA 2378
Qy 3020 GCCACTGTAACAGGATTAGCAGAGCAGGATGCTAGCGGTGCTACAGAGTCTTGAAG 3079
Db 2379 GCCACTGTAACAGGATTAGCAGAGCAGGATGCTAGCGGTGCTACAGAGTCTTGAAG 2438
Qy 3080 TGTGGCTTAACCTACCGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAG 3139
Db 2439 TGTGGCTTAACCTACCGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAG 2498
Qy 3140 CCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATTCGGGCAAAACAAACCGCTGGT 3199
Db 2499 CCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATTCGGGCAAAACAAACCGCTGGT 2558
Qy 3200 AGCGGTGTTTTTTTGTTCAGACGACAGATACGCGCAGAAAGGATCTCAAGAA 3259
Db 2559 AGCGGTGTTTTTTTGTTCAGACGACAGATACGCGCAGAAAGGATCTCAAGAA 2618
Qy 3260 GATCCTTTGATCTTTTCTACGGGCTGTGACGCTCAGTGGGAACGAAACTCACGTTAAGGG 3319
Db 2619 GATCCTTTGATCTTTTCTACGGGCTGTGACGCTCAGTGGGCTCTGACGC----- 2650
Qy 3320 ATTTTGTGATGAGCGGATACATATTTGAATGATTTAGAAAAATAACAAATAGGGGTT 3379
Db 2651 ----- 2650
Qy 3380 CCGCGCACATTTCCCGAAAGTGCCACCTGTATGCGGTGTGAATACCGCACAGATGCG 3439
Db 2651 ----- 2650

Qy 3440 TAAGGAGAAATACCGCATCAGGAATTTGTAAGCGTTAATAATTCAGAGAACTCGTCAA 3499
Db 2651 -----TCAGAGAACTCGTCAA 2667
Qy 3500 GAAGGCGATAGAAGCGATGCGCTGCGAAATCGGGAGCGGATACCGTAAAGACACGAGGA 3559
Db 2668 GAAGGCGATAGAAGCGATGCGCTGCGAAATCGGGAGCGGATACCGTAAAGACACGAGGA 2727
Qy 3560 AGCGGTGAGCCCAATTCGCGCCCAAGCTCTTCAGCAATATCACGGGTAGCCAAACGCTATGT 3619
Db 2728 AGCGGTGAGCCCAATTCGCGCCCAAGCTCTTCAGCAATATCACGGGTAGCCAAACGCTATGT 2787
Qy 3620 CCTGATAGCGGTGCGCCACACCCAGCGGCAACAGTCCGATGAATCCAGAAAAAGCGGCAT 3679
Db 2788 CCTGATAGCGGTGCGCCACACCCAGCGGCAACAGTCCGATGAATCCAGAAAAAGCGGCAT 2847
Qy 3680 TTTTCCACCATGATATTCGGCAAGCAGCATCGCCATGGGTACGACGACGAGATCTTCGCGCT 3739
Db 2848 TTTTCCACCATGATATTCGGCAAGCAGCATCGCCATGGGTACGACGAGATCTTCGCGCT 2907
Qy 3740 CGGGCATGCTCGCGCTTGAGCCTGGCGCAACAGTTGCGGTGGCGGAGCCCTGATGCTCTT 3799
Db 2908 CGGGCATGCGCGCTTGAGCCTGGCGCAACAGTTGCGGTGGCGGAGCCCTGATGCTCTT 2967
Qy 3800 CGTCCAGATCATCTGATCGACAAAGACCGGCTTCCATCCGAGTACGTCGCTCGATGTC 3859
Db 2968 CGTCCAGATCATCTGATCGACAAAGACCGGCTTCCATCCGAGTACGTCGCTCGATGTC 3027
Qy 3860 GATGTTTCGCTTGGTTCGAATGGGCAAGTACGCGATCAAGGATGATGAGAGATCCT 3919
Db 3028 GATGTTTCGCTTGGTTCGAATGGGCAAGTACGCGATCAAGGATGATGAGAGATCCT 3087
Qy 3920 TTCATCAGCCATGATGAGTACTTTCTCGCAGGAGCAAGGTGAGATGACAGAGATCCT 3979
Db 3088 TTCATCAGCCATGATGAGTACTTTCTCGCAGGAGCAAGGTGAGATGACAGAGATCCT 3147
Qy 3980 GCCCGCGCATTCGCGCAATAGCAGCAGTCCCTTCCCGCTTCAGTGACAAACGTCGAGCA 4039
Db 3148 GCCCGCGCATTCGCGCAATAGCAGCAGTCCCTTCCCGCTTCAGTGACAAACGTCGAGCA 3207
Qy 4040 CAGTGGCGAAGAAACCGCGCTGTCGCGCAGCCACAGATAGCCGCTGCTCTTGCA 4099
Db 3208 CAGTGGCGAAGAAACCGCGCTGTCGCGCAGCCACAGATAGCCGCTGCTCTTGCA 3267
Qy 4100 GTTCATTTCAGGGCACCGGACAGGTCGCTTTGACAAAAAGAACCCGGCGCCCTGCGCTG 4159
Db 3268 GTTCATTTCAGGGCACCGGACAGGTCGCTTTGACAAAAAGAACCCGGCGCCCTGCGCTG 3327
Qy 4160 ACAGCCGGAACACCGCGGATCAGAGCAGCCGATTTGCTGTTGTCAGTTCATAGCCGA 4219
Db 3328 ACAGCCGGAACACCGCGGATCAGAGCAGCCGATTTGCTGTTGTCAGTTCATAGCCGA 3387
Qy 4220 ATAGCTCTCCACCCAGCGCGGAGAACCTCGGTGCAATCCATCTTGTTCATATGTC 4279
Db 3388 ATAGCTCTCCACCCAGCGCGGAGAACCTCGGTGCAATCCATCTTGTTCATATGTC 3447
Qy 4280 GAAACCATCTCATCTGCTCTTGTATCAGAGCTTGTATCCCTCGCGCATCAG 4332
Db 3448 GAAACCATCTCATCTGCTCTTGTATCAGATCTTGTATCCCTCGCGCATCAG 3500

RESULT 3
BD136051

LOCUS
DEFINITION
Interferon alpha plasmid and delivery system and method of
preparing and using the same.

ACCESSION
BD136051
VERSION
BD136051.1 GI:23230996
KEYWORDS
JP 2002506647-A/18.
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.

BD136051 3589 bp DNA linear PAT 18-SEP-2002

REFERENCE	1 (bases 1 to 3589)
AUTHORS	Norderstrom,J., Pericle,F., Rolland,A. and Ralston,R.
TITLE	Interferon alpha plasmid and delivery system and method of preparing and using the same
JOURNAL	Patent: JP 2002506647-A 18 05-MAR-2002;
COMMENT	VALENTIS INC OS Artificial Sequence PN JP 2002506647-A/18 PD 05-MAR-2002 PF 12-MAR-1999 JP 2000536861 PR 19-NAR-1998 US 60/078654 PI JEFF NORDSTROM, FEDERICA PERICLE, ALAIN ROLLAND, ROBERT RALSTON PC C12N15/09,A61K38/21,A61K48/00,A61P35/00,C07K14/54,C07K14/56, PC C12N1/15, PC C12N1/19,C12N1/21,C12N5/10//A61K9/127,C12N15/00,A61K37/66, PC C12N5/00
FEATURES	CC Sequence source: synthetic construct FH Key Location/Qualifiers FT source 1..3589 /organism='Artificial Sequence'. FT Location/Qualifiers 1..3589 /organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630"
ORIGIN	
	Query Match 44.4%; Score 1923.8; DB 6; Length 3589; Best Local Similarity 72.2%; Pred. No. 0; Matches 2897; Conservative 0; Mismatches 603; Indels 512; Gaps 10
QY	321 CGTTACATAACTTACGGTAATGGCCGCTTGCGTAGCAGCCCAACGACCCCGGCCCATTT 380
Db	1 CGTTACATPACTTACGGTAATGGCCGCTTGCGTAGCAGCCCAACGACCCCGGCCCATTT 60
QY	381 GACGTCAAATAATGACGTATGTTCCATAGTAACGCCTAATAGGGAATTCCTTCATTGACGTCA 440
Db	61 GACGTCAAATAATGACGTATGTTCCATAGTAACGCCTAATAGGGAATTCCTTCATTGACGTCA 120
QY	441 ATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGATCATCATATGCC 500
Db	121 ATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGATCATCATATGCC 180
QY	501 AAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCTTGGCATTTATGCCAGTA 560
Db	181 AAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCTTGGCATTTATGCCAGTA 240
QY	561 CATGACCTTATGGGACTTTCTCTACTTTGGCAGTACATCTACGTATTAGTCATCGCTATTAC 620
Db	241 CATGACCTTATGGGACTTTCTCTACTTTGGCAGTACATCTACGTATTAGTCATCGCTATTAC 300
QY	621 CATGTGTATGCGGTTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGAATCACGGGG 680
Db	301 CATGTGTATGCGGTTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGAATCACGGGG 360
QY	681 ATTTCCAAGTCTCCACCCTTACAGCTCAATGGGAGTTTGTTTTGGSCACAAAATCAACG 740
Db	361 ATTTCCAAGTCTCCACCCTTACAGCTCAATGGGAGTTTGTTTTGGSCACAAAATCAACG 420
QY	741 GGACTTTCCAAATGTCGTAAACAATCCGCCCTTACGCCAAATGGGCGGTAGGCGTGT 800
Db	421 GGACTTTCCAAATGTCGTAAACAATCCGCCCTTACGCCAAATGGGCGGTAGGCGTGT 480
QY	801 ACGGTGGGAGGCTATATAAGCAGAGCTCGTTTAGTGAAACCGTCAGATCGCTTGGAGACG 860
Db	481 ACGGTGGGAGGCTATATAAGCAGAGCTCGTTTAGTGAAACCGTCAGATCGCTTGGAGACG 540
QY	861 CCATCCACGCTTTTTGACCTCCATAGAGACACCGGACCGGATCCAGGCTGACTCTAGC 920
Db	541 CCATCCACGCTTTTTGACCTCCATAGAGACACCGGACCGGATCCAGGCTGACTCTAGC ----- 589
QY	921 CTAGCTCTGAAAGTTGGTGTGTAGGGCCCTCGGCGACGGTTGGTATCAAGGTTTACAGACAGGT 980

Db 3389 ||||| TAGCCTCTCCACCAAGCGCGGAGAACCTGCGTGCAAATCCATCTTGTTCAATCATGCG 3448
Qy 4281 AAAGCATCCTCATCCTGCTCTCTTGATCAGAGCTTGATCCCTGCGCCATCAG 4332
Db 3449 AAACGATCCTCATCCTGCTCTCTTGATCAGATCTTGATCCCTGCGCCATCAG 3500

RESULT 4
AR260588 8349 bp DNA linear PAT 20-DEC-2002
LOCUS AR260588
DEFINITION Sequence 16 from patent US 6489542.
ACCESSION AR260588
VERSION AR260588.1 GI:27311143
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 8349)
AUTHORS Corbin,D.R. and Romano,C.P.
TITLE Methods for transforming plants to express Cry2Ab
-delta.-endotoxins targeted to the plastids
JOURNAL Patent: US 6489542-A 16 03-DEC-2002;
Monsanto Technology LLC; St. Louis, MO
FEATURES
source Location/Qualifiers
1..8349
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 42.6%; Score 1845.4; DB 6; Length 8349;
Best Local Similarity 92.6%; Pred. No. 0;
Matches 1983; Conservative 0; Mismatches 101; Indels 57; Gaps 2;

Qy 2249 AGCTTGGCGTAATCATGTGTCATAGCTGTTTCTGTGTGAATGTTATCCGTCACAATT 2308
Db 5909 AGCTTGGCGTAATCATGTGTCATAGCTGTTTCTGTGTGAATGTTATCCGTCACAATT 5969

Qy 2309 CCACAACAATACAGCGCGGAGCATAAAGTGTAAAGCGCTGGGTGTCCTAATGAGTGAGC 2368
Db 5969 CCACAACAATACAGCGCGGAGCATAAAGTGTAAAGCGCTGGGTGTCCTAATGAGTGAGC 6028

Qy 2369 TAACTCAATTAATTTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGC 2428
Db 6029 TAACTCAATTAATTTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGC 6088

Qy 2429 CAGCTGCATTAATGAATCGGCAACCGCGGGGAGAGCGGTTTCGCTATTGGGCGCTCT 2488
Db 6089 CAGCTGCATTAATGAATCGGCAACCGCGGGGAGAGCGGTTTCGCTATTGGGCGCTCT 5148

Qy 2489 TCCGCTTCCCTCGCTCACTGACTCGCTGCGCTCGGTGCTGCGTGGCGAGCGGTATCA 2548
Db 6149 TCCGCTTCCCTCGCTCACTGACTCGCTGCGCTCGGTGCTGCGTGGCGAGCGGTATCA 6208

Qy 2549 GCTCACTAAAGCGGTAATAGCTGTTATCCAGATCAGGGATAACGCGAGAAAGAC 2608
Db 6209 GCTCACTAAAGCGGTAATAGCTGTTATCCAGATCAGGGATAACGCGAGAAAGAC 6268

Qy 2609 ATGTGAGCAAAAGGCGCAGCAAGGCGAGAAACCGTAAAGGCGCGTGTGCGGCTT 2668
Db 6269 ATGTGAGCAAAAGGCGCAGCAAGGCGAGAAACCGTAAAGGCGCGTGTGCGGCTT 6328

Qy 2669 TTCCATAGGCTCCGCCCTCGACGAGCATCAAAAATCGAGCTCAAGTCAGAGGTGG 2728
Db 6329 TTCCATAGGCTCCGCCCTCGACGAGCATCAAAAATCGAGCTCAAGTCAGAGGTGG 6388

Qy 2729 CGAAACCCGACGAGACTATAAGATACAGGCGTTTCCCGCTGGAGCTCCCTCGTGGCG 2788
Db 6389 CGAAACCCGACGAGACTATAAGATACAGGCGTTTCCCGCTGGAGCTCCCTCGTGGCG 6448

Qy 2789 TCTCTGTTCCGACCTGCGCTTACCGGATACCTGTCGCGCTTTTCCCTTCGGGAAGC 2848
Db 6449 TCTCTGTTCCGACCTGCGCTTACCGGATACCTGTCGCGCTTTTCCCTTCGGGAAGC 6508

Qy 2849 GTGGCGCTTTCTCAATGCTCAAGCTGTAGGTATCTCAAGTTCGGTGTAGGTCGTTGCTCC 2908
Db 6509 GTGGCGCTTTCTCAATGCTCAAGCTGTAGGTATCTCAAGTTCGGTGTAGGTCGTTGCTCC 6568

Qy 2909 AAGCTGGGCTGTGTGACAGAACCCCGCTTACGCCCGACCGCTGCGCTTATCCGCTAAC 2968
Db 6569 AAGCTGGGCTGTGTGACAGAACCCCGCTTACGCCCGACCGCTGCGCTTATCCGCTAAC 6628

Qy 2969 TATCGTCTCAGTCCAAACCGGTAAAGACAGCATTTATCGCCACTTGGCAGCAGCCACTGGT 3028
Db 6629 TATCGTCTCAGTCCAAACCGGTAAAGACAGCATTTATCGCCACTTGGCAGCAGCCACTGGT 6688

Qy 3029 AACAGATATAGCAGAGGATGTAGGCGGTCTACAGATTTCTTGAAGTGTGGCT 3088
Db 6689 AACAGATATAGCAGAGGATGTAGGCGGTCTACAGATTTCTTGAAGTGTGGCT 6748

Qy 3089 AACTACGCTACACTAGAGGACAGATTTTGGTATCTGCGCTCTGCTGAACGAGTTACC 3148
Db 6749 AACTACGCTACACTAGAGGACAGATTTTGGTATCTGCGCTCTGCTGAACGAGTTACC 6808

Qy 3149 TTCCGAAAAAGAGTTGGTAGCTCTTGTATCCGGCAAAACAAACCAACCGCTGGTAGCGGTGGT 3208
Db 6809 TTCCGAAAAAGAGTTGGTAGCTCTTGTATCCGGCAAAACAAACCAACCGCTGGTAGCGGTGGT 6868

Qy 3209 TTTTGTGTGCAAGCAGCAGATTAACGGCAGAAAAAAGATCTCAAGAGATCTTTTG 3268
Db 6869 TTTTGTGTGCAAGCAGCAGATTAACGGCAGAAAAAAGATCTCAAGAGATCTTTTG 6928

Qy 3269 ATCTTTTCTACGGGCTCTGACGCTCAGTGGAAACGAAATCTCAGTTAAGGATTTTGTC 3328
Db 6929 ATCTTTTCTACGGGCTCTGACGCTCAGTGGAAACGAAATCTCAGTTAAGGATTTTGTC 6988

Qy 3329 ATGAGCGGATACATATTGAAATGATTTTGA----- 3359
Db 6989 ATGAGATTAACAAAAGGATCTTCACTAGATCTCTTTTGGGTGGGCGAAGAACTCCAGC 7048

Qy 3360 -----AAAATAAAATAAGGTTCCGGGACATTTCCCGAAAAAG 3401
Db 7049 ATGAGATCCCGCGCTGGAGGATCATCAGCGCGGCTCCCGAAAAACGATTTCCGAAGCCC 7108

Qy 3402 TGCCACCTGTATCGGTG-----TGAAATACCGCACAGATGCTTAAGGAGAAAT 3451
Db 7109 AACCTTTCATAGAGCGCGGTGGAATCGAAATCTCTGTATGGCAGGTTGGCGCTCGCT 7168

Qy 3452 ACCGCATCAGGAAATTTGAGCGTTAATAATTCAAGAAATCTGTCAGAGGCGCATAGA 3511
Db 7169 TGGTCGGTCAITTTGAAACCCAGAGTCCCGCTCAGAGAACTCGTCAAGAGGCGCATAGA 7228

Qy 3512 AGGCGATCGCTGCGAATCGGGAGCGGATACCGTAAAGCAGCAGGAGCGGTCAAGCCC 3571
Db 7229 AGGCGATCGCTGCGAATCGGGAGCGGATACCGTAAAGCAGCAGGAGCGGTCAAGCCC 7288

Qy 3572 ATTCCCGCGCAAGCTCTTTCAGCAATATCAAGGATAGCCAAAGCTATGCTGATAGCGGT 3631
Db 7289 ATTCCCGCGCAAGCTCTTTCAGCAATATCAAGGATAGCCAAAGCTATGCTGATAGCGGT 7348

Qy 3632 CCGCCACACCCAGCGGCGCACAGTCAGTGAATTCAGAAAGCGGCGCATTTTCCACCATGA 3691
Db 7349 CCGCCACACCCAGCGGCGCACAGTCAGTGAATTCAGAAAGCGGCGCATTTTCCACCATGA 7408

Qy 3692 TATTCCGCAAGCAGGCGCATCGGTCACGACGATCTCTCGCGCTGGGCGATCTCG 3751
Db 7409 TATTCCGCAAGCAGGCGCATCGGTCACGACGATCTCTCGCGCTGGGCGATCTCGGCG 7468

Qy 3752 CTTTGAGCTGCGCAACAGTTCCGGTGGCGGAGCCCTTGATGCTCTTCTCGATCAT 3811
Db 7469 CTTTGAGCTGCGCAACAGTTCCGGTGGCGGAGCCCTTGATGCTCTTCTCGATCAT 7528

Qy 3812 CTTGATTCGACAGACCGGCTTCCATCCGAGTACGTCCTCGATGCGATGTTTCGCTT 3871
Db 7529 CTTGATTCGACAGACCGGCTTCCATCCGAGTACGTCCTCGATGCGATGTTTCGCTT 7588


```
Qy 3872 GGTGGTCAATGGGACAGTATGCGGATCAAGCGTATGACGCGCGCGCAATTGCATCAGCCA 3931
Db 7589 GGTGGTCAATGGGACAGTATGCGGATCAAGCGTATGACGCGCGCGCAATTGCATCAGCCA 7648
Qy 3932 TGATGGATACCTTCTCGGACGAGCAAGGTGAGATGACAGAGATCTCTGCCCCGGCACTT 3991
Db 7649 TGATGGATACCTTCTCGGACGAGCAAGGTGAGATGACAGAGATCTCTGCCCCGGCACTT 7708
Qy 3992 CGCCCAATAGCAGCAGTCCCTTCCCGCTTCCAGTGACAAAGTGCAGACACAGCTGCGCAAG 4051
Db 7709 CGCCCAATAGCAGCAGTCCCTTCCCGCTTCCAGTGACAAAGTGCAGACACAGCTGCGCAAG 7768
Qy 4052 GAACGCCCGTGTGGCCAGCACATAGCCGCTGCTCTGTCTTGCAAGTTCATTCAGGG 4111
Db 7769 GAACGCCCGTGTGGCCAGCACATAGCCGCTGCTCTGTCTTGCAAGTTCATTCAGGG 7828
Qy 4112 CACCGGACAGTGGTCTTGACAAAAGAACCGGCGCGCTGCGCTGACAGCGCGGAACA 4171
Db 7829 CACCGGACAGTGGTCTTGACAAAAGAACCGGCGCGCTGCGCTGACAGCGCGGAACA 7888
Qy 4172 CGGCGGCATCAGACAGCCGATCTCTGTGTGCGCCAGTATAGCCGAATAGCTCTCCA 4231
Db 7889 CGGCGGCATCAGACAGCCGATCTCTGTGTGCGCCAGTATAGCCGAATAGCTCTCCA 7948
Qy 4232 CCCAAGCGCGGAGAACCTCGGTGCAATCCATCTTGTTCATCATCGCAACGATCCTC 4291
Db 7949 CCCAAGCGCGGAGAACCTCGGTGCAATCCATCTTGTTCATCATCGCAACGATCCTC 8008
Qy 4292 ATCTGTCTTGTATGACAGTTCATCCCTGCGCCATCAG 4332
Db 8009 ATCTGTCTTGTATGACAGTTCATCCCTGCGCCATCAG 8049

RESULT 5
SYN8KMRG/c
LOCUS SYN8KMRG 2661 bp DNA linear SYN 27-APR-1993
DEFINITION Synthetic plasmid pK18 (pBRNeo/pUC18) kanamycin resistance gene,
complete cds.
ACCESSION M17626
VERSION M17626.1 GI:207845
KEYWORDS complete genome; kanamycin resistance.
SOURCE unidentified cloning vector
ORGANISM unidentified cloning vector
other sequences; artificial sequences; vectors.
REFERENCE 1 (bases 1 to 2661)
AUTHORS Pridmore,R.D.
TITLE New and versatile cloning vectors with kanamycin-resistance marker
JOURNAL Gene 56 (2-3), 309-312 (1987)
PUBMED 3315864
COMMENT Original
FEATURES
    source
        1..2661
            /organism="unidentified cloning vector"
            /mol_type="genomic DNA"
            /db_xref="taxon:45196"
            365..1159
            /note="kanamycin"
            /codon_start=1
            /transl_table=11
            /protein_id="AAA72612.1"
            /db_xref="GI:207846"
            /translations="MTEQDLGAGSPAAWVERLFGVDWAQQTIGCSDAAVFRLSAQGR
            PVLFVKTDLSGALNEQDEAARLSWLTATGVPVCAVLDVVTEAGRWLLIGVPGQDL
            LSSHLPAEKVSIWADMRRLHLDPATCFDPAKHRIERARTRMEAGLVDDDDDE
            EHQGLAPAEILFARKAMPDGEDLVVTHGDACLPNIWENGRESGIFDCGRUGVADRY
            QDIALATRDIAELGGEWADRFLVLVGIAPDSQRIAFYRLLEPF"
    CDS
        1..2661
            /protein_id="AAA72612.1"
            /db_xref="GI:207846"
            /translations="MTEQDLGAGSPAAWVERLFGVDWAQQTIGCSDAAVFRLSAQGR
            PVLFVKTDLSGALNEQDEAARLSWLTATGVPVCAVLDVVTEAGRWLLIGVPGQDL
            LSSHLPAEKVSIWADMRRLHLDPATCFDPAKHRIERARTRMEAGLVDDDDDE
            EHQGLAPAEILFARKAMPDGEDLVVTHGDACLPNIWENGRESGIFDCGRUGVADRY
            QDIALATRDIAELGGEWADRFLVLVGIAPDSQRIAFYRLLEPF"
    ORIGIN
        42.4%; Score 1836.8; DB 11; Length 2661;
        Best Local Similarity 92.5%; Pred. No. 0;
        Matches 1975; Conservative 0; Mismatches 102; Indels 57; Gaps 2;
        Qy 2256 CGTAATCATGGTCATAGCTGTTCTCTGTGTGAATTTGTTATCGCTCACAAATCCACACA 2315
```

```
Db 2443 CGTAATCATGGTCATAGCTGTTCTCTGTGTGAATTTGTTATCCGCTCACAAATCCACACA 2384
Qy 2316 ACATACGAGCGGAGAGCATAAAGTGTAAAGCTTGGGTGCTTAATGATGAGCTAACTCA 2375
Db 2383 ACATACGAGCGGAGAGCATAAAGTGTAAAGCTTGGGTGCTTAATGATGAGCTAACTCA 2324
Qy 2376 CATTAATTGGTGTGGCTCACTCGCCGCTTTCAGATCGGGAAACCTGTCTGTCGACGTGC 2435
Db 2323 CATTAATTGGTGTGGCTCACTCGCCGCTTTCAGATCGGGAAACCTGTCTGTCGACGTGC 2264
Qy 2436 ATTAATGAATTCGGCCAAACGCGCGGGAGAGCGGTTTGCGTATTTGGCGCTCTTTCCGCTT 2495
Db 2263 ATTAATGAATTCGGCCAAACGCGCGGGAGAGCGGTTTGCGTATTTGGCGCTCTTTCCGCTT 2204
Qy 2496 CCTCGCTCACTGACTCGCTCGCTCGGTTCGTTTGGGTGCGGCGAGCGGTATCAGTCACT 2555
Db 2203 CCTCGCTCACTGACTCGCTCGCTCGGTTCGTTTGGGTGCGGCGAGCGGTATCAGTCACT 2144
Qy 2556 CAAAGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACGACAGGAAAGAAACATGTGAG 2615
Db 2143 CAAAGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACGACAGGAAAGAAACATGTGAG 2084
Qy 2616 CAAAGCGCCAGCAAAAGGCGCAGAACCGTAAAAAGCGCGCTTCTCGCGCTTTTCCATA 2675
Db 2083 CAAAGCGCCAGCAAAAGGCGCAGAACCGTAAAAAGCGCGCTTCTCGCGCTTTTCCATA 2024
Qy 2676 GGCTCGCGCCCTCGTACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGGAAACC 2735
Db 2023 GGCTCGCGCCCTCGTACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGGAAACC 1964
Qy 2736 CGACAGGACTATAAAGATACAGCGCTTCCCGCTGGAAGCTCCCTCGTGGCTCTCTCGT 2795
Db 1963 CGACAGGACTATAAAGATACAGCGCTTCCCGCTGGAAGCTCCCTCGTGGCTCTCTCGT 1904
Qy 2796 TTCCGACCTGCGCTTACCGGATACTGTGCGCTTTCTCCCTTCCGGAAGCGGTGGCGC 2855
Db 1903 TTCCGACCTGCGCTTACCGGATACTGTGCGCTTTCTCCCTTCCGGAAGCGGTGGCGC 1844
Qy 2856 TTCTCTCAATGCTCAACGCTGTAGTATCTCAGTTTGGGTGATGCTGCTGCTCCAGCTGG 2915
Db 1843 TTCTCTCAATGCTCAACGCTGTAGTATCTCAGTTTGGGTGATGCTGCTGCTCCAGCTGG 1784
Qy 2916 GCTGTGTGACGAAACCCCGCTTTCAGCCCGCTGCGCTTATCCGCTAACTATCGTC 2975
Db 1783 GCTGTGTGACGAAACCCCGCTTTCAGCCCGCTGCGCTTATCCGCTAACTATCGTC 1724
Qy 2976 TTGAGTCCAAACCCCGGTAAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGA 3035
Db 1723 TTGAGTCCAAACCCCGGTAAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGA 1664
Qy 3036 TTAGCAGAGCGAGTATAGCGGTGCTACAGATTTCTTGAAGTGGTGGCTTAACCTACG 3095
Db 1663 TTAGCAGAGCGAGTATAGCGGTGCTACAGATTTCTTGAAGTGGTGGCTTAACCTACG 1604
Qy 3096 GCTACACTAGAAGACAGATTTTGGTATCTGCGCTCTGCTGTAAGCCAGTTTACCTTCGGAA 3155
Db 1603 GCTACACTAGAAGACAGATTTTGGTATCTGCGCTCTGCTGTAAGCCAGTTTACCTTCGGAA 1544
Qy 3156 AAGAGTTGGTAGCTTGTATCCGGCAAAACCAACCGCTGCTAGCGGTGGTTTTTTT 3215
Db 1543 AAGAGTTGGTAGCTTGTATCCGGCAAAACCAACCGCTGCTAGCGGTGGTTTTTTT 1484
Qy 3216 TTTGCAAGCAGCAGATTTACGCGCAGAAAAAAGGATCTCAAGAAAGATCTCTTTGATCTTTT 3275
Db 1483 TTTGCAAGCAGCAGATTTACGCGCAGAAAAAAGGATCTCAAGAAAGATCTCTTTGATCTTTT 1424
Qy 3276 CTACGCGGTGTCAGCTCAGTGGAAACGAAACCTCAGCTTAAGGGAATTTGGTCAATGACG 3335
Db 1423 CTACGCGGTGTCAGCTCAGTGGAAACGAAACCTCAGCTTAAGGGAATTTGGTCAATGAGAT 1364
Qy 3336 GATACATATTGTAATGATTTTGA----- 3359
```

```
Db 1363 TATCAAAAGGATCTTCACTAGATCCTTTTGGGGTGGCGAAGAACTCCAGCATGAGAT 1304
Qy 3360 -----AAATAAACAATAGGGTTCCGGCACATTTCCCGGAAAGTGCACAC 3408
Db 1303 CCCCGCGCTGGAGATCATCAGCGCGGTCCCGGAAACGATTCGAGCCCACTTT 1244
Qy 3409 TGTATGGGTG-----TGAATACCCACAGATGCGTAAAGAGAGAAATACCGCAT 3458
Db 1243 CATAGAAGCGCGGTGGAATCGAATCTCGTATGCGAGGTGGCGTGCCTTGGTGG 1184
Qy 3459 CAGGAATTTGAAGCTTAATAATTCAGAGAACTCGTCAAGAGAGGATAGAAGGCAT 3518
Db 1183 TCATTTGCAACCCAGAGTCCCGCTCAGAGAACTCGTCAAGAGAGGCGATAGAAGGCAT 1124
Qy 3519 GCGCTGGAANTCGGAGCGGCGATACGTAAGACAGGAGGAGCGGTGAGCCCATTCGCC 3578
Db 1123 GCGCTGCAATCGGAGCGGCGATACCGTAAGACAGGAGGAGCGGTGAGCCCATTCGCC 1064
Qy 3579 GCCAAGCTCTTCAGCAATATCACGGGTAGCCAAAGCTATGTCTCTATAGCGGTCCGCCAC 3638
Db 1063 GCCAAGCTCTTCAGCAATATCACGGGTAGCCAAAGCTATGTCTCTATAGCGGTCCGCCAC 1004
Qy 3639 ACCGAGCGGCGCACAGTGCATGAATTCAGAGAAAGCGGCCATTTCCACCATGATATCGG 3698
Db 1003 ACCGAGCGGCGCACAGTGCATGAATTCAGAGAAAGCGGCCATTTCCACCATGATATCGG 944
Qy 3699 CAAGCAGGCATCGCCATCGGTACAGCAGATCTCGCGCTGGGCGATGCTCGCTTGAG 3758
Db 943 CAAGCAGGCATCGCCATCGGTACAGCAGATCTCGCGCTGGGCGATGCTCGCTTGAG 884
Qy 3759 CCGTGGCAACAGTTCGGCTGGCGAGCCCTGATGCTCTTCTGCTCAGATCATCTGATC 3818
Db 883 CCGTGGCAACAGTTCGGCTGGCGAGCCCTGATGCTCTTCTGCTCAGATCATCTGATC 824
Qy 3819 GACAAAGCGGTTCCATCGAGTACGTCGCTCGATGCGATGCTTGGCTTGGTGTC 3878
Db 823 GACAAAGCGGTTCCATCGAGTACGTCGCTCGATGCGATGCTTGGCTTGGTGTC 764
Qy 3879 GAATCGGAGGTAGCGGATCAAGCGTATGAGCGCGCGCATGTCATCAGCCATGATGGA 3938
Db 763 GAATCGGAGGTAGCGGATCAAGCGTATGAGCGCGCGCATGTCATCAGCCATGATGGA 704
Qy 3939 TACTTTCTCGGAGGACAGGTGAGATGACAGGAGATCTGCGCGGCACTTCGCCCAA 3998
Db 703 TACTTTCTCGGAGGACAGGTGAGATGACAGGAGATCTGCGCGGCACTTCGCCCAA 644
Qy 3999 TAGCAGCCAGTCCCTTCCGCTTCAGTGACAGCTGAGCAGCTGCGCAGGAAAGCC 4058
Db 643 TAGCAGCCAGTCCCTTCCGCTTCAGTGACAGCTGAGCAGCTGCGCAGGAAAGCC 584
Qy 4059 CGTCTGGCGCAGCCAGTAGCGGCTGCTCGTCTTGCAGTTCATTTCAGGCGCACCGGA 4118
Db 583 CGTCTGGCGCAGCCAGTAGCGGCTGCTCGTCTTGCAGTTCATTTCAGGCGCACCGGA 524
Qy 4119 CAGGTGCGTCTTGACAAAAGAACCGGGCGCCCTGCGCTGACAGCCGGAACACGCGGC 4178
Db 523 CAGGTGCGTCTTGACAAAAGAACCGGGCGCCCTGCGCTGACAGCCGGAACACGCGGC 464
Qy 4179 ATCAGAGCAGCGATGCTGTTGTGCGCCAGTCATAGCCGATAGCTCTCCACCCAGC 4238
Db 463 ATCAGAGCAGCGATGCTGTTGTGCGCCAGTCATAGCCGATAGCTCTCCACCCAGC 404
Qy 4239 GCGCGGAGAACCTGCGTGAATCCATCTTGTTCATATGCGAAACGATCCTCATCTGT 4298
Db 403 GCGCGGAGAACCTGCGTGAATCCATCTTGTTCATATGCGAAACGATCCTCATCTGT 344
Qy 4299 CTCCTGATCAGAGCTTGTCCCTGCGCCATCAG 4332
Db 343 CTCCTGATCAGATCTTGTATCCCTGCGCCATCAG 310
```

```
LOCUS SYNCCDBA 2999 bp DNA linear SYN 16-MAR-2000
DEFINITION Cloning vector pKil118 ccdB gene, complete cds and
kanamycin-resistance (Kmr) gene fragment.
ACCESSION L38498
VERSION L38498.1 GI:986977
KEYWORDS ccdB gene; cloning vector; kanamycin resistance.
SOURCE Cloning vector pKil118
ORGANISM Cloning vector pKil118
REFERENCE 1 (bases 1 to 2999)
AUTHORS Bernard P.
TITLE New ccdB positive-selection cloning vectors with kanamycin or
chloramphenicol selectable markers
JOURNAL Gene 162 (1), 159-160 (1995)
PUBMED 7557407
FEATURES             Location/Qualifiers
     source           1..2999
                     /organism="Cloning vector pKil118"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:118286"
     gene             1..381
                     /gene="ccdB"
     CDS              1..381
                     /gene="ccdB"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="AAC42103.1"
                     /db_xref="GI:986978"
                     /translation="MTWITNSSVPGDPLESTCRHASLSLQFKYVYTKRESRYRLFVD
                     VQSDIIDTPGRWVPIPLASARLLDKVSRELYPVVHHGDESRRWMTTDMASVPVSVIG
                     EVADLSHRENDIKNAINLMPWGI"
ORIGIN
Query Match      42.1%; Score 1821.8; DB 11; Length 2999;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 1960; Conservative 0; Mismatches 102; Indels 57; Gaps 2;
Qy 2271 AGCTGTTTCTGTTGAAATTTGTTATCCGCTCACATATCCACACATACGAGCGCGAA 2330
Db 2999 AGCTGTTTCTGTTGAAATTTGTTATCCGCTCACATATCCACACATACGAGCGCGAA 2940
Qy 2331 GCATAAAGTAAAGCCCTGGGTGCTAATCAGTGAGCTAACTCACATTAATTTGGTTGC 2390
Db 2939 GCATAAAGTAAAGCCCTGGGTGCTAATCAGTGAGCTAACTCACATTAATTTGGTTGC 2880
Qy 2391 GCTCACTCCCGCTTTCCAGTCCGGAACCTGTGCTGCCAGTCAATTAATGAATCGGCC 2450
Db 2879 GCTCACTCCCGCTTTCCAGTCCGGAACCTGTGCTGCCAGTCAATTAATGAATCGGCC 2820
Qy 2451 AACGCGCGGAGAGCGGTTTGGTATTTGGCGCTCTTCCGCTTCCCTCGCTCACTGACT 2510
Db 2819 AACGCGCGGAGAGCGGTTTGGTATTTGGCGCTCTTCCGCTTCCCTCGCTCACTGACT 2760
Qy 2511 CGTCCGCTCGCTCGCTTCCGCTTCCGCTGCGAGCGGTATCAGTCACTCAAAGCGGTAATAC 2570
Db 2759 CGCTCGCTCGCTCGCTTCCGCTGCGAGCGGTATCAGTCACTCAAAGCGGTAATAC 2700
Qy 2571 GGTATTACAGAAATCAGGGGATAACGAGGAAGAAACATGTGAGCAAAAGGCCAGCAAA 2630
Db 2699 GGTATTACAGAAATCAGGGGATAACGAGGAAGAAACATGTGAGCAAAAGGCCAGCAAA 2640
Qy 2631 AGGCCAGGAACCGTAAAGCGCGTTCCTGGCGCTTTTCCATAGGCTCCGCCCCCTCG 2690
Db 2639 AGGCCAGGAACCGTAAAGCGCGTTCCTGGCGCTTTTCCATAGGCTCCGCCCCCTCG 2580
Qy 2691 ACAGCATCACAAAATCGACGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAA 2750
Db 2579 ACAGCATCACAAAATCGACGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAA 2520
Qy 2751 GATACAGCGGTTTCCCTCGTGAAGCTCCCTGCGGCTCTCTGTTCGACCCCTGCCGC 2810
Db 2519 GATACAGCGGTTTCCCTCGTGAAGCTCCCTGCGGCTCTCTGTTCGACCCCTGCCGC 2460
```


Matches 1960; Conservative				0; Mismatches	102; Indels	57; Gaps	2;
Qy	2271	AGCTGTTTCTCTGTGTGAAATTTGTTATTCGCGTCACAATTCACACAAACATACGAGCCGAA	2330				
Db	2999	AGCTGTTTCTCTGTGTGAAATTTGTTATTCGCGTCACAATTCACACAAACATACGAGCCGAA	2940				
Qy	2331	GCATAAGTGTAAGCCTGGGGTGCCTAATGATGAGTGAGCTAACTCACTAATTAATTTGCGTTGC	2390				
Db	2939	GCATAAAGTGTAAGCCTGGGGTGCCTAATGATGAGTGAGCTAACTCACTAATTAATTTGCGTTGC	2880				
Qy	2391	GCTCACTGCCCGCTTCCAGTCCGGGAAAACCTGTCGCCAGCTGCATTAATGAATCGGCC	2450				
Db	2879	GCTCACTGCCCGCTTCCAGTCCGGGAAAACCTGTCGCCAGCTGCATTAATGAATCGGCC	2820				
Qy	2451	AACGCGCGGGAGAGCGGTTTCGTTATTTGGGCGCTCTTCGCTCTCTCGCTCACTGACT	2510				
Db	2819	AACGCGCGGGAGAGCGGTTTCGTTATTTGGGCGCTCTTCGCTCTCTCGCTCACTGACT	2760				
Qy	2511	CGCTGCCTCGGTCGTTTCGCGTCCGGAGCGGTATCAGTCACTCAAAAGCGGTAAATAC	2570				
Db	2759	CGCTGCCTCGGTCGTTTCGCGTCCGGAGCGGTATCAGTCACTCAAAAGCGGTAAATAC	2700				
Qy	2571	GGTTATCCACAGAATCAGGGGATAACGACGAAAGAACATGTGAGCAAAAGGCCAGCAAA	2630				
Db	2699	GGTTATCCACAGAATCAGGGGATAACGACGAAAGAACATGTGAGCAAAAGGCCAGCAAA	2640				
Qy	2631	AGGCCAGAACCGTAATAAAGCGCGCTTGTCTGGCGTTTTCATAGGCTCCGCCCCCTG	2690				
Db	2639	AGGCCAGAACCGTAATAAAGCGCGCTTGTCTGGCGTTTTCATAGGCTCCGCCCCCTG	2580				
Qy	2691	ACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGGAAACCGACGAGCACTATAA	2750				
Db	2579	ACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGGAAACCGACGAGCACTATAA	2520				
Qy	2751	GATACACAGCGTTTCCCTCGGAAAGTCCCTCGTGCGCTCTCTGTTCCGACCTGCCGC	2810				
Db	2519	GATACACAGCGTTTCCCTCGGAAAGTCCCTCGTGCGCTCTCTGTTCCGACCTGCCGC	2460				
Qy	2811	TTACGGGATACCTGTCGCGCTTTCCTCTTCGGGAAGCGTGGCGCTTCTCAATGCTCAC	2870				
Db	2459	TTACGGGATACCTGTCGCGCTTTCCTCTTCGGGAAGCGTGGCGCTTCTCAATGCTCAC	2400				
Qy	2871	GCTGTAGTATCTCAGTTTCGGTGTAGTCTCGCTCCAGTCTGGGCTGTGTGCACGAAC	2930				
Db	2399	GCTGTAGTATCTCAGTTTCGGTGTAGTCTCGCTCCAGTCTGGGCTGTGTGCACGAAC	2340				
Qy	2931	CCCCGTTTCAGCCGACCGCTTATCCGTTAACTATCGTCTTGAGTCAACCCCG	2990				
Db	2339	CCCCGTTTCAGCCGACCGCTTATCCGTTAACTATCGTCTTGAGTCAACCCCG	2280				
Qy	2991	TAAGACACGACTTATCGCACTGGCAGCAGCACTGGTAAACAGATTTAGCAGAGCGAGT	3050				
Db	2279	TAAGACACGACTTATCGCACTGGCAGCAGCACTGGTAAACAGATTTAGCAGAGCGAGT	2220				
Qy	3051	ATGTAGGCGGTGTACAGAGTTCTTGAAGTGTGCGCTTAACACGCTACACTAGAGGA	3110				
Db	2219	ATGTAGGCGGTGTACAGAGTTCTTGAAGTGTGCGCTTAACACGCTACACTAGAGGA	2160				
Qy	3111	CAGTATTTGGTATCTCGGCTCTGCTGAAGCCAGTTTACCTTCGAAAAAGAGTTGGTAGCT	3170				
Db	2159	CAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTTACCTTCGAAAAAGAGTTGGTAGCT	2100				
Qy	3171	CTTGATCCGGCAAAACAAACCCGCTGGTAGCGGTGTTTTTTTTTTTGTTCAGACGAGA	3230				
Db	2099	CTTGATCCGGCAAAACAAACCCGCTGGTAGCGGTGTTTTTTTTTTTGTTCAGACGAGA	2040				
Qy	3231	TTACGCGCAGAAAAAAGAGTCTCAAGAAAGTCTTTTGTGATCTTTTCTACGGGGTCTCAGC	3290				
Db	2039	TTACGCGCAGAAAAAAGAGTCTCAAGAAAGTCTTTTGTGATCTTTTCTACGGGGTCTCAGC	1980				
Qy	3291	CTCAGTGGAAACGAAACTCACGTTAAGGATTTTTGGTCAATGAGCGGATACATATTTGAAT	3350				
Db	1979	CTCAGTGGAAACGAAACTCACGTTAAGGATTTTTGGTCAATGAGATTTATCAAAAAGGATCT	1920				

QY	3351	GTATTTAGA-----AAAA	3366	
DB	1919	TCACCTAGATTCCTTTTGGGTGGCGAAGAACTCCAGCATGAGATCCC	CGCGCTGGAGGA	1860
QY	3364	TAAACAATAAGGGTTC	CGCGCACATTTCCCGAAAAGTCCACCTGTATGCGGTG----	3419
DB	1859	TCATCCAGCGGGTCCCGGAAAA	CGATTCGGAAGCCCAACCTTTTCATAGAAGCGGCGG	1800
QY	3420	-----TGA	AATACCGCACAGATGCGTATAGGAGAAAATACCGCATCAGAAATTTGTAAGC	3473
DB	1799	TGGAATCGAAATCTCGTGATGGCAGGTGGGCGTCGCTTGGTCGGTCA	TTTTCGAAACCCCA	1740
QY	3474	GTTTAATAATTCAGAGA	AACTCGTCAAGAGGCGCATAGAAAGGCGATCGCTGCGAAATCGGG	3533
DB	1739	GAGTCCCGCTCAGA	GAAGAACTTCGTCAAGAGGCGCATAGAAAGGCGATGGCTGCGAAATCGGG	1680
QY	3534	AGCGCGGATACCGTAA	AGCAAGGAGCGGTTCAGCCCATTCGCCGCAAGTCTTTTCAGC	3593
DB	1679	AGCGCGGATACCGTAA	AGCAAGGAGCGGTTCAGCCCATTCGCCGCAAGTCTTTTCAGC	1620
QY	3594	AATATACAGGGTAGCCAA	CGCTATGCTTCATAGCGGTTCGCCACACCCAGCGCGGCACA	3653
DB	1619	AATATACAGGGTAGCCAA	CGCTATGCTTCATAGCGGTTCGCCACACCCAGCGCGGCACA	1560
QY	3654	GTCCGATGAATCCAGAAA	AGCGGCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCC	3713
DB	1559	GTCCGATGAATCCAGAAA	AGCGGCATTTTTCACCATGATATTCGGCAAGCAGGCATCGCC	1500
QY	3714	ATGGGTCA	CGACGAGATCTTCGCCGTCGGGCGATGCTCGCTTCAGCGCTTGGCGAACAGTTTC	3773
DB	1499	ATGGGTCA	CGACGAGATCTTCGCCGTCGGGCGATGCTCGCTTCAGCGCTTGGCGAACAGTTTC	1440
QY	3774	GGCTGGCGGAGCCCTGATGCTCTTCGTCACAGATCATCTCTGATCGACA	AGACCGGCTTC	3833
DB	1439	GGCTGGCGGAGCCCTGATGCTCTTCGTCACAGATCATCTCTGATCGACA	AGACCGGCTTC	1380
QY	3834	CATCCGAGTAGCTGCTCGCTCGATTCGATGCTTTCGCTTGGTGGTTCGAAT	GGGCGAGGTGAC	3893
DB	1379	CATCCGAGTAGCTGCTCGCTCGATTCGATGCTTTCGCTTGGTGGTTCGAAT	GGGCGAGGTGAC	1320
QY	3894	CGGATCAAGCGTATCGACGCGCCCGCATTCATCAGCCATCATGATGATGAT	TTCTTCGGCAGG	3953
DB	1319	CGGATCAAGCGTATCGACGCGCCCGCATTCATCAGCCATCATGATGATGAT	TTCTTCGGCAGG	1260
QY	3954	AGCAAGGTGAGATGACAGGAGATCTTCGCCCGGCACTTCGCCCAATAGCAGC	CAAGTCCCT	4013
DB	1259	AGCAAGGTGAGATGACAGGAGATCTTCGCCCGGCACTTCGCCCAATAGCAGC	CAAGTCCCT	1200
QY	4014	TCCCGCTTCAGTGACAAGCTCGACGACAGCTGCGCAAGGAACGCCCTCTG	TGGCGACGCCA	4073
DB	1199	TCCCGCTTCAGTGACAAGCTCGACGACAGCTGCGCAAGGAACGCCCTCTG	TGGCGACGCCA	1140
QY	4074	CGATAGCCCGCTGCTGCTTCAGTTCAATTCAGGGCACCGGACAGGTTCGT	CTTTGAC	4133
DB	1139	CGATAGCCCGCTGCTGCTTCAGTTCAATTCAGGGCACCGGACAGGTTCGT	CTTTGAC	1080
QY	4134	AAAAAGAACCGGGCGCCCTCGCTGTCAGCGCGGAACACGCGCGCATCAGAG	CAAGCGAT	4193
DB	1079	AAAAAGAACCGGGCGCCCTCGCTGTCAGCGCGGAACACGCGCGCATCAGAG	CAAGCGAT	1020
QY	4194	TGTCGTGTTGCGCCAGTCA	TAGCCGAATAGCTCTCCACCAAGCGCGCGAGAACCTTCG	4253
DB	1019	TGTCGTGTTGCGCCAGTCA	TAGCCGAATAGCTCTCCACCAAGCGCGCGAGAACCTTCG	960
QY	4254	GTGCAATCCATCTTGTTC	CAATCATCGGAAACGATCCTCATCTCTTGCATCAGAGCT	4313
DB	959	GTGCAATCCATCTTGTTC	CAATCATCGGAAACGATCCTCATCTCTTGCATCAGAGCT	900
QY	4314	TGATCCCTTGGCGCATTCAG	4332	
DB	899	TGATCCCTTGGCGCATTCAG	881	

RESULT 8		2959 bp DNA		circular SYN 10-APR-2002	
AF402779	LOCUS	2959 bp DNA	circular SYN 10-APR-2002		
DEFINITION	Expression vector pKSUc1, complete sequence.				
ACCESSION	AF402779				
VERSION	AF402779.1	GI:15290650			
KEYWORDS					
SOURCE	ORGANISM				
REFERENCE	1 (bases 1 to 2959)				
AUTHORS	Kolisnychenko, V., Plunkett, G. III, Herring, C.D., Feher, T., Posfai, J., Blattner, F.R. and Posfai, G.				
TITLE	Engineering a reduced Escherichia coli genome				
JOURNAL	Genome Res. 12 (4), 640-647 (2002)				
PUBMED	11932248				
REFERENCE	2 (bases 1 to 2959)				
AUTHORS	Posfai, G.				
TITLE	Direct Submission				
JOURNAL	Submitted (25-JUL-2001) Biochemistry, Biological Research Center, Temesvari Krt., 62, Szeged 6701, Hungary				
FEATURES	Location/Qualifiers				
source	1..2959				
	/organism="Expression vector pKSUc1"				
	/mol_type="genomic DNA"				
	/specific_host="Escherichia coli"				
	/db_xref="taxon:169791"				
gene	120..821				
	/gene="I-sceI"				
CDS	120..821				
	/gene="I-sceI"				
	/codon_start=1				
	/transl_table=11				
	/product="I-SceI meganuclease"				
	/protein_id="AAK94924.1"				
	/db_xref="GI:15290651"				
	/translation="MQKQVNMGNLSPNSKLLKEYKYSQLEINTEQFEAGIGLIGDAY				
	IRSDQETCMQFQWKNKAYMDHCVLLYDQVLSPPHKRVRNHGLNVLVTWGAQTF				
	KHQAFKNLANLFIVNNKTIIPNNLVENLYTPMSLAFYFMDGDKGNDYNNKSNKSVL				
	NTQSFTPEEVEYLVGKLRNKFQNLVCYKINKKPIIIVDSMSYLIFFNLIKPYLIQPM				
	MYKLPTNISSETFLK"				
gene	complement (2014..2808)				
	/gene="kan"				
CDS	complement (2014..2808)				
	/gene="kan"				
	/codon_start=1				
	/transl_table=11				
	/product="kanamycin phosphotransferase"				
	/protein_id="AAK94925.1"				
	/db_xref="GI:15290652"				
	/translation="MIEQDLGSHGSPAANVERLFGYDMAQQTIGCSDAAVFRLSAQR				
	PLVLFKTDLSGALNEQDEARLSLWATTPGCAAVLDVVRTEAGRDMLLIGVEPGDGL				
	LSLHAPAEKVSIMADMRHLHTLPATCFPHQAKHRIERATRMEAGLVDDDDLDE				
	EHQGLAPAEIAPLARKMPDGEDLVVTHGDACLPMIENVENGPSFGIDCGRLGVADRY				
	QDIALATRDIAEELGGEWADRFLVLYGIAAPDSQRIAFYRLLEDFP"				
ORIGIN					
Query Match	42.0%; Score 1817.8; DB 11; Length 2959;				
Best Local Similarity	93.9%; Pred. No. 0;				
Matches 1938; Conservative	0; Mismatches 62; Indels 63; Gaps 2;				
QY	2245	TTCCAGCTTGGCGTATCATGGTTCATAGCTGTTTCTGTGTGAAATGTTATCCGCTCAC	2304		
Db	839	TGCAAGCTTGGCGTAATCATGGTTCATAGCTGTTTCTGTGTGAAATGTTATCCGCTCAC	898		
QY	2305	AATTCCACACAAATATTCGGTTGGCGTCACTGCCCGCTTTTCAGTTCGGGAAACCTGTC	2364		
Db	899	AATTCCACACACATAGACGCCGGAAGCATAAAGTGTAAAGCTTGGGTGCCTTAATGAGT	958		
QY	2365	GAGCTTAATCACAATTAATTCGGTTGGCGTCACTGCCCGCTTTTCAGTTCGGGAAACCTGTC	2424		
Db	959	GAGCTTAATCACAATTAATTCGGTTGGCGTCACTGCCCGCTTTTCAGTTCGGGAAACCTGTC	1018		

QY 3505 CGATAGAGCGATGCGCTGCGATCGGAGCGCGGATACCGTAAACACAGAGAACGG 3564
 Db 2036 CGATAGAGCGATGCGCTGCGATCGGAGCGCGGATACCGTAAACACAGAGAACGG 2095
 QY 3565 TCAGCCCATTCGCGCGCAAGCTCTTACGCAATATCAGCGGTAGCAGCGTATGCTCTGA 3624
 Db 2096 TCAGCCCATTCGCGCGCAAGCTCTTACGCAATATCAGCGGTAGCAGCGTATGCTCTGA 2155
 QY 3625 TAGCGGTCCGCCACACCCAGCGCGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTC 3684
 Db 2156 TAGCGGTCCGCCACACCCAGCGCGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTC 2215
 QY 3685 ACCATGATATTGGCAAGCAGCGATCGCATGGGTACGACGATCTCGCCCTCGGCG 3744
 Db 2216 ACCATGATATTGGCAAGCAGCGATCGCATGGGTACGACGATCTCGCCCTCGGCG 2275
 QY 3745 ATGCTCGCTTGAGCTGGCGAAGCAGTTCCGCTGGCGGAGCCCTGATGCTCTGCTCC 3804
 Db 2276 ATCGCGCTTTGAGCTGGCGAAGCAGTTCCGCTGGCGGAGCCCTGATGCTCTGCTCC 2335
 QY 3805 AGATCATCTGATCGACAAGACCGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGT 3864
 Db 2336 AGATCATCTGATCGACAAGACCGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGT 2395
 QY 3865 TTGCGTTGGTGGTCCGAATGGCAGGTAGCCGGAATCAAGCGTATGACGCGCGCATTTGCA 3924
 Db 2396 TTGCGTTGGTGGTCCGAATGGCAGGTAGCCGGAATCAAGCGTATGACGCGCGCATTTGCA 2455
 QY 3925 TCAGCCATGATGATATTTCTCGCAGGAGCAGGTGATGATGATGATGATGATGATGATG 3984
 Db 2456 TCAGCCATGATGATATTTCTCGCAGGAGCAGGTGATGATGATGATGATGATGATGATG 2515
 QY 3985 GGCACTTCGCCCAATAGCAGCAGCTCCCTTCCGCTTCCAGTACAAACCGTCGACACAGCT 4044
 Db 2516 GGCACTTCGCCCAATAGCAGCAGCTCCCTTCCGCTTCCAGTACAAACCGTCGACACAGCT 2575
 QY 4045 GCGCAAGGAACGCCGCTCGTGCCAGCCACGATAGCCGCGTGCCTGCTTTGCGAGTTCA 4104
 Db 2576 GCGCAAGGAACGCCGCTCGTGCCAGCCACGATAGCCGCGTGCCTGCTTTGCGAGTTCA 2635
 QY 4105 TTCAGGACCGGACAGCTCGTCTTGACAAAAGAACCGGCGCCCTGCGCTGACAGC 4164
 Db 2636 TTCAGGACCGGACAGCTCGTCTTGACAAAAGAACCGGCGCCCTGCGCTGACAGC 2695
 QY 4165 CGGAACAGCGCGCATCAGACAGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4224
 Db 2696 CGGAACAGCGCGCATCAGACAGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2755
 QY 4225 CTCTCCACCCAGCGCGGAGAACCTGCGTCAATTCATCTTTGTTCAATCATGCGAAGC 4284
 Db 2756 CTCTCCACCCAGCGCGGAGAACCTGCGTCAATTCATCTTTGTTCAATCATGCGAAGC 2815
 QY 4285 GATCTCATCTGCTCTCTTGATC 4307
 Db 2816 GATCTCATCTGCTCTCTTGATC 2838

RESULT 9
 LOCUS AY189826/c 2604 bp DNA circular SYN 09-APR-2003
 DEFINITION His-3 integration vector pJHAM001, complete sequence.
 ACCESSION AY189826
 VERSION AY189826.1 GI:28435536
 KEYWORDS his-3 integration vector pJHAM001
 SOURCE his-3 integration vector pJHAM001
 ORGANISM his-3 integration vector pJHAM001
 other sequences; artificial sequences; vectors.
 REFERENCE 1 (bases 1 to 2604)
 AUTHORS Lee,D.W., Haag,J.R. and Aramayo,R.
 TITLE Construction of strains for rapid homokaryon purification after
 integration of constructs at the histidine-3 (his-3) locus of
 Neurospora crassa
 JOURNAL Curr. Genet. 43 (1), 17-23 (2003)

12684841
 2 (bases 1 to 2604)
 AUTHORS Lee,D.W., Haag,J.R. and Aramayo,R.
 TITLE Direct Submission
 JOURNAL Submitted (03-DEC-2002) Biology, Texas A&M University, BSBW 415,
 College Station, TX 77843-3258, USA
 FEATURES
 Location/Qualifiers
 1..2604
 /organism="his-3 integration vector pJHAM001"
 /mol_type="genomic DNA"
 /db_xref="taxon:220724"
 /note="modified pK18 vector"
 misc_feature
 2542..2572
 /note="modified multi-cloning site"
 ORIGIN
 Query Match 41.1%; Score 1780.8; DB 11; Length 2604;
 Best Local Similarity 92.3%; Pred. No. 0;
 Matches 1931; Conservative 0; Mismatches 102; Indels 59; Gaps 3;
 QY 2298 CGCTCACAATTCACAAACATACGAGCGGAGACATAAAGTGTAAAGCCTGGGGTGCCT 2357
 Db 2542 CGCTCACAATTCACAAACATA--AGCGGAGACATAAAGTGTAAAGCCTGGGGTGCCT 2485
 QY 2358 AATGAGTGAGTAACTCACAATTAATTCGCTTGCCTCACTGCCCGCTTCCAGTCGGAA 2417
 Db 2484 AATGAGTGAGTAACTCACAATTAATTCGCTTGCCTCACTGCCCGCTTCCAGTCGGAA 2425
 QY 2418 ACCTGTCTGCGAGCTGCAATTAATTCGCGCCAAACGCGGGGAGAGCGGTTTGCCTA 2477
 Db 2424 ACCTGTCTGCGAGCTGCAATTAATTCGCGCCAAACGCGGGGAGAGCGGTTTGCCTA 2365
 QY 2478 TTGGGCGCTCTTCGCTTCTCGCTCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2537
 Db 2364 TTGGGCGCTCTTCGCGCTTCTCGCTCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTG 2305
 QY 2538 GAGCGGTATCAGCTCAGTCAAAAGCGGTAATACGTTATCCACAGAAATCAGGGGATAACG 2597
 Db 2304 GAGCGGTATCAGCTCAGTCAAAAGCGGTAATACGTTATCCACAGAAATCAGGGGATAACG 2245
 QY 2598 CAGGAAAGAACATGTGAGCAAAAGCCAGCAAAAGCCAGGAAACCGTAAAAAGCGCGCT 2657
 Db 2244 CAGGAAAGAACATGTGAGCAAAAGCCAGCAAAAGCCAGGAAACCGTAAAAAGCGCGCT 2185
 QY 2658 TGCTGGCGTTTTCATAGGCTCCGCCCTGCTGAGCAGCATCAGAAATTCAGCGCTCAA 2717
 Db 2184 TGCTGGCGTTTTCATAGGCTCCGCCCTGCTGAGCAGCATCAGAAATTCAGCGCTCAA 2125
 QY 2718 GTCAGAGTGGGAAACCCGACAGGACTATAAAGATACAGGCGTTTCCCGCTGGAAGCT 2777
 Db 2124 GTCAGAGTGGGAAACCCGACAGGACTATAAAGATACAGGCGTTTCCCGCTGGAAGCT 2065
 QY 2778 CCCTCTGCGCTCTCTCTGTTCCGACCCCTGCTGCGGATACTGTCGCGCTTTCTCTCC 2837
 Db 2064 CCCTCTGCGCTCTCTCTGTTCCGACCCCTGCTGCGGATACTGTCGCGCTTTCTCTCC 2005
 QY 2838 CTTCCGGAAGCGTGGCGCTTCTCAATGCTCAGCTGATAGTATCTCAGTTCGCTGATAG 2897
 Db 2004 CTTCCGGAAGCGTGGCGCTTCTCAATGCTCAGCTGATAGTATCTCAGTTCGCTGATAG 1945
 QY 2898 TCGTTTCGCTCCAAAGCTGGGCTGTGTCACGAAACCCCGCTTTCAGCCCGACCGCTGCGCT 2957
 Db 1944 TCGTTTCGCTCCAAAGCTGGGCTGTGTCACGAAACCCCGCTTTCAGCCCGACCGCTGCGCT 1885
 QY 2958 TATCCGGAATATCTGCTTTGAGTCCAAACCCCGGTAGACACGACTTATGCCACTGGCAG 3017
 Db 1884 TATCCGGAATATCTGCTTTGAGTCCAAACCCCGGTAGACACGACTTATGCCACTGGCAG 1825
 QY 3018 CAGCCACTGGTAAACAGGATTACGAGCGGATGTATGCTAGCGGTGCTACAGAGTTCTTGA 3077
 Db 1824 CAGCCACTGGTAAACAGGATTACGAGCGGATGTATGCTAGCGGTGCTACAGAGTTCTTGA 1765
 QY 3078 AGTGGTGGCTAACTACGCTACACTAGAGGACAGTATTTGGTATCTCGGCTCTGCTGTA 3137

```
Db 1764 AGTGGTGGCTAACTACGGCTACACTAGAGGACAGTATTGGTATCTGGCTCTGCTGA 1705
Qy 3138 AGCCAGTACCTTCGGAAAAAGAGTGGTAGCTCTTGATCGGCAAAACAACACCCGCTG 3197
Db 1704 AGCCAGTACCTTCGGAAAAAGAGTGGTAGCTCTTGATCGGCAAAACAACACCCGCTG 1645
Qy 3198 GTACGGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTTACGCGCAGAAAAAAGGATCTCAAG 3257
Db 1644 GTACGGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTTACGCGCAGAAAAAAGGATCTCAAG 1585
Qy 3358 AAGATCCTTTGATCTTTTCTACCGGGTCTGACGCTCAGTGGAACGAAAACTCAGTTAAG 3317
Db 1584 AAGATCCTTTGATCTTTTCTACCGGGTCTGACGCTCAGTGGAACGAAAACTCAGTTAAG 1525
Qy 3318 GGATTTGGTTCATGAGCGGATACATATTGATGATTATAGA----- 3359
Db 1524 GGATTTGGTTCATGAGATTATCAAAAAGGATCTTTCACCTAGATCTTTTGGGGTGGCGGA 1465
Qy 3360 -----AAAATAAAATAAGGGTTCGCGCACATT 3390
Db 1464 AGAATCCAGATGAGATCCCGCGCTGGAGGATCATCCAGCGCGGTCCCGGAAACGA 1405
Qy 3391 TCCCGGAAAAGTGCCACTGATCGGTG-----TGAATACCGCACAGATCGGT 3440
Db 1404 TTCCGAAGCCCAACTTTTCATAGAAGCGCGGTGGAATCGAATCTCGTATGGCAGGT 1345
Qy 3441 AAGGAGAAATACCGATCAGGAATTTGTAAGCGTTAATATTAGAAAGTCTGTCAG 3500
Db 1344 TGGCGGTGCGTGTGTCGCTCATTTTCGAACCCAGAGTCCCGCTCAGAAGAACTCGTCAAG 1285
Qy 3501 AAGCGGATAGAAGCGGATGCGCTCGGAATCGGAGCGCGGATACCGTAAAGCAGAGGAA 3560
Db 1284 AAGCGGATAGAAGCGGATGCGCTCGGAATCGGAGCGCGGATACCGTAAAGCAGAGGAA 1225
Qy 3561 GCGGTGAGCCCATTTGCGCGCAAGCTTTTCAGCAATATCAGGATAGCCAAACGCTATGTC 3620
Db 1224 GCGGTGAGCCCATTTGCGCGCAAGCTTTTCAGCAATATCAGGATAGCCAAACGCTATGTC 1165
Qy 3621 CTGATAGCGGTCCGCAACCCAGCGCGGCACAGTCGATGATGATCCAGAAAGCGGCATT 3680
Db 1164 CTGATAGCGGTCCGCAACCCAGCGCGGCACAGTCGATGATGATCCAGAAAGCGGCATT 1105
Qy 3681 TTCCACCATGATATTCGGCAAGCAGGATCGCCATCGGTACAGCAGAGATCTTCGCGCTC 3740
Db 1104 TTCCACCATGATATTCGGCAAGCAGGATCGCCATCGGTACAGCAGAGATCTTCGCGCTC 1045
Qy 3741 GGGCATGCTCGCTTGAGCTTGGCGAAACAGTTGCGCTGGCGCGAGCCCTGATGCTCTTC 3800
Db 1044 GGGCATCGCGCTTGAGCTTGGCGAAACAGTTGCGCTGGCGCGAGCCCTGATGCTCTTC 985
Qy 3801 GTCAGATCATCTGATCGACAGACCGGCTTCATCCGAGTACGTCTGCTCGTATGCG 3860
Db 984 GTCCAGATCATCTGATCGACAGACCGGCTTCATCCGAGTACGTCTGCTCGTATGCG 925
Qy 3861 ATGTTTCGCTTGGTGGTTCGAATGGCGAGGTAGCGGATCAAGCTGATGCGAGCCCGCAT 3920
Db 924 ATGTTTCGCTTGGTGGTTCGAATGGCGAGGTAGCGGATCAAGCTGATGCGAGCCCGCAT 865
Qy 3921 TGCATCAGCCATGATGATATCTTCTCGGCAAGGAGGATGAGATCAAGGAGATCCTG 3980
Db 864 TGCATCAGCCATGATGATATCTTCTCGGCAAGGAGGATGAGATCAAGGAGATCCTG 805
Qy 3981 CCCCGGCACTTCGCCCAATAGCAGCGGATCCCTTCGCTTCAGTACGACAGCTGAGCAC 4040
Db 804 CCCCGGCACTTCGCCCAATAGCAGCGGATCCCTTCGCTTCAGTACGACAGCTGAGCAC 745
Qy 4041 AGCTGCGCAAGAAACGCGCTGCTGGCGCAGCAGATAGCGGCTGCTCTGCTTCGAG 4100
Db 744 AGCTGCGCAAGAAACGCGCTGCTGGCGCAGCAGATAGCGGCTGCTCTGCTTCGAG 685
Qy 4101 TTCAATTAGGGCACCGGACAGGTGCGTCTTGA CAAAAAGAAACCGGGCGCCCTCGCGTGA 4160
```

```
Db 684 TTCAATTCAGGGCACCGACAGGTGCGTCTTGACAAAAAGAACCGGGCGCCCTCGCGTGA 625
Qy 4161 CAGCCGGAACACCGCGGCATCAGAGCAGCGGATGCTGTGTGTCGCCAGTCATAGCCGAA 4220
Db 624 CAGCCGGAACACCGCGGCATCAGAGCAGCGGATGCTGTGTGTCGCCAGTCATAGCCGAA 565
Qy 4221 TAGCCTCTCCACCACCAAGCGCGGAGAACCTGCGTGAATCCATCTTGTTCATCATGCG 4280
Db 564 TAGCCTCTCCACCACCAAGCGCGGAGAACCTGCGTGAATCCATCTTGTTCATCATGCG 505
Qy 4281 AAACGATCTTCATCTCTCTCTTGTGATCAGAGCTTGATCCCTCGCGCATCAG 4332
Db 504 AAACGATCTTCATCTCTCTCTTGTGATCAGATCTTGATCCCTCGCGCATCAG 453

RESULT 10
AY189827/c
LOCUS 11373 bp DNA circular SYN 09-APR-2003
DEFINITION His-3 integration vector pJHAM002, complete sequence.
ACCESSION AY189827
VERSION AY189827.1 GI:28435537
KEYWORDS
SOURCE
ORGANISM
his-3 integration vector pJHAM002
other sequences; artificial sequences; vectors.
REFERENCE
1 (bases 1 to 11373)
Lee,D.W., Haag,J.R. and Aramayo,R.
Construction of strains for rapid homokaryon purification after
integration of constructs at the histidine-3 (his-3) locus of
Neurospora crassa
Curr. Genet. 43 (1), 17-23 (2003)
JOURNAL
PUBMED 12684841
REFERENCE
2 (bases 1 to 11373)
Lee,D.W., Haag,J.R. and Aramayo,R.
Direct Submission
TITLE
Submitted (03-DEC-2002) Biology, Texas A&M University, BSBW 415,
College Station, TX 77843-3258, USA
JOURNAL
FEATURES
Location/Qualifiers
source 1..11373
/organism="his-3 integration vector pJHAM002"
/mol_type="genomic DNA"
/db_xref="taxon:220725"
/focus
source 1..2597
/organism="his-3 integration vector pJHAM001"
/mol_type="genomic DNA"
/db_xref="taxon:220724"
misc_feature 2598..11373
/notes="his-3 HindIII fragment"
misc_feature 6156..6183
/notes="multi-cloning sites"
ORIGIN
Query Match 41.1%; Score 1780.8; DB 11; Length 11373;
Best Local Similarity 92.3%; Pred. No. 0;
Matches 1931; Conservative 0; Mismatches 102; Indels 59; Gaps 3;
Qy 2298 CGCTCAATTCACACACATACGAGCCGAGAGCATAAAGTGTAAAGCTGGGTGCTT 2357
Db 2574 CGCTCAATTCACACACATTAATTTGGTGGCTCACTGCCGCTTTCAGTCGGGAA 2517
Qy 2358 AATGAGTGAGTAACTCACAATTAATTTGGTGGCTCACTGCCGCTTTCAGTCGGGAA 2417
Db 2516 AATGAGTGAGTAACTCACAATTAATTTGGTGGCTCACTGCCGCTTTCAGTCGGGAA 2457
Qy 2418 ACTGTGTCGAGCTGCAATTAATGAATCGGCAACGCGCGGAGAGCGGTTTGGCTA 2477
Db 2456 ACCTGTGTCGAGCTGCAATTAATGAATCGGCAACGCGCGGAGAGCGGTTTGGCTA 2397
Qy 2478 TTGGGCGCTCTTCGCTTCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGGC 2537
Db 2396 TTGGGCGCTCTTCGCTTCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGGC 2337
```

QY	2538	GAGCGGTATCAGCTCACTCAAAAGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACG	2597
DB	2336	GAGCGGTATCAGCTCACTCAAAAGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACG	2277
QY	2598	CAGGAAGACATGTGAGCAAAAGCCGCAAAAGGCCAGGACCGTAAAAAGCCGCGT	2657
DB	2276	CAGAAAGAACATGTGAGCAAAAGCCGCAAAAGGCCAGGAAACCGTAAAAAGCCGCGT	2217
QY	2658	TGTCGGCGTTTTTCCATAGGCTCCGCGCCCTGACGAGCATCAAAAAATCGACGCTCAA	2717
DB	2216	TGTCGGCGTTTTTCCATAGGCTCCGCGCCCTGACGAGCATCAAAAAATCGACGCTCAA	2157
QY	2718	GTCAAGGTGGCAAAACCGACAGACTATAAGATACCAAGCGTTTCCCCCTGGAGCT	2777
DB	2156	GTCAAGGTGGCAAAACCGACAGACTATAAGATACCAAGCGTTTCCCCCTGGAGCT	2097
QY	2778	CCCTCGTGCCTCTCTCTGTTCCGACCTCGCGCTTACCGGATACCTGTCCGCTTTCTCC	2837
DB	2096	CCCTCGTGCCTCTCTCTGTTCCGACCTCGCGCTTACCGGATACCTGTCCGCTTTCTCC	2037
QY	2838	CTTCGGAAAGGTGGCGCTTTCTCAATGCTCAAGTGTAGGTATCTCAGTTCTGGTGTAGG	2897
DB	2036	CTTCGGAAAGGTGGCGCTTTCTCAATGCTCAAGTGTAGGTATCTCAGTTCTGGTGTAGG	1977
QY	2898	TGCTTCGCTCCAAAGCTGGGCTGTGACAGAAACCCCGGTTACAGCCGACCGCTCGCCT	2957
DB	1976	TGCTTCGCTCCAAAGCTGGGCTGTGACAGAAACCCCGGTTACAGCCGACCGCTCGCCT	1917
QY	2958	TATCCGGTAACTATCGTCTTGAGTCCAAACCGGTAAAGACAAGATATGCCACTGGCAG	3017
DB	1916	TATCCGGTAACTATCGTCTTGAGTCCAAACCGGTAAAGACAAGATATGCCACTGGCAG	1857
QY	3018	CAGCCACTGTATAACAGAAATAGCAGCGAGGTATGTAGCGGTGTCTACAGAGTCTTGA	3077
DB	1856	CAGCCACTGTATAACAGAAATAGCAGCGAGGTATGTAGCGGTGTCTACAGAGTCTTGA	1797
QY	3078	AGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTGTATCTCGCTCTCTCGA	3137
DB	1796	AGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTGTATCTCGCTCTCTCGA	1737
QY	3138	AGCAGATTACCTTCGGAAAAAGAGTGGTGTAGTCTTTGATCCGGGAAACAAACACCGCTG	3197
DB	1736	AGCAGATTACCTTCGGAAAAAGAGTGGTGTAGTCTTTGATCCGGGAAACAAACACCGCTG	1677
QY	3198	GTAGCGGTGGTTTTTTTTTTGTTGCAAGCAGCAGATTACGCCAGAAAAAAGGATCTCAAG	3257
DB	1676	GTAGCGGTGGTTTTTTTTTTGTTGCAAGCAGCAGATTACGCCAGAAAAAAGGATCTCAAG	1617
QY	3258	AAGATTCCTTTGATCTTTTCTACGGGGTCTGACCGTCTAGTGGAAACGAAAACTCAGTTAAG	3317
DB	1616	AAGATTCCTTTGATCTTTTCTACGGGGTCTGACCGTCTAGTGGAAACGAAAACTCAGTTAAG	1557
QY	3318	GGATTTTGGTCAACGCGGATACATATTTGAAATGATTTAGA-----	3359
DB	1556	GGATTTTGGTCAACGCGGATACATATTTGAAATGATTTAGA-----	1497
QY	3360	-----	3390
DB	1496	AGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCGCGCTCCGGAAAAACGA	1437
QY	3391	TCCCGGAAAAGTGCCACTGTATCGGGTG-----TGAATACCGCACAGATCGCT	3440
DB	1436	TTCGGAAGCCCAACTTTTCATAGAAGGCGCGGTGGAAATCGAAATCTCGTGTGGCAGGT	1377
QY	3441	AAGGAGAAAAATACCGCATACGGAATAATGTAAGCGCTTAATAATTCAGAAGAACTCGTCAAG	3500
DB	1376	TGGCGCTCGCTTGTTCGCTCATTTCCGAACCCAGAGTCCCGCTCAGAAGAACTCGTCAAG	1317
QY	3501	AAGCGGATAGAAAGCGATGCGCTCGGAATCGGAGCGCGGATACCGTAAAGCAGAGAA	3560
DB	1316	AAGCGGATAGAAAGCGATGCGCTCGGAATCGGAGCGCGGATACCGTAAAGCAGAGAA	1257
QY	3561	CGCGTCAGCCCAATTCGCGCCCAAGCTCTTTCAGCAATATCACGGGTAGCCAACTGTGTC	3620

[illegible]

AUTHORS	TITLE
Lee, D. W., Haag, J. R. and Aramayo, R.	Construction of strains for rapid homokaryon purification after integration of constructs at the histidine-3 (his-3) locus of

JOURNAL
Neurospora crassa
Curr. Genet. 43 (1), 17-23 (2003)

PUBMED
12684841
2 (bases 1 to 11403)

AUTHORS Lee,D.W.; Haag,D.R. and Aramayo,K.
TITLE Direct Submission
JOURNAL Submitted (03-DEC-2002) Biology, T

TITLE
Direct submission
Submitted (03-DEC-2002) Biology, Texas A&M University, BSBW 415,
JOURNAL

FEATURES	College Station, TX 77843-3258, USA
source	Location/Qualifiers 1. .11403 /organism="his-3 integration vector pJHAM004" /mol_type="genomic DNA" /db_xref="taxon:220727" /locus
source	1. .2597 /organism="his-3 integration vector pJHAM001" /mol_type="genomic DNA" /db_xref="taxon:220724" 2598. .11403 /note="his-3 HindIII fragment" 7793. .7845 /note="multi-cloning sites"
misc_feature	
misc_feature	
ORIGIN	
Query Match	41.1%; Score 1780.8; DB 11; Length 11403;
Best Local Similarity	92.3%; Pred. No. 0;
Matches 1931; Conservative	0; Mismatches 102; Indels 59; Gaps 3;
Qy	2298 CGCTCAAAATTCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTTGGGGTGCCT 2357
Db	2574 CGCTCAAAATTCACACACACATA--AGCCGAAGCATAAAGTGTAAAGCCTTGGGGTGCCT 2517
Qy	2358 AATGAGTGAGCTAACTCACATTAATTGGTTGCCTCACTGCCCGCTTTCAGTTCGGGAA 2417
Db	2516 AATGAGTGAGCTAACTCACATTAATTGGTTGCCTCACTGCCCGCTTTCAGTTCGGGAA 2457
Qy	2418 ACCTGTCTGTCAGCTGATTAATGAATCGGCCAAACGCGGGGAGAGGCGGTTTGCCTA 2477
Db	2456 ACCTGTCTGTCAGCTGATTAATGAATCGGCCAAACGCGGGGAGAGGCGGTTTGCCTA 2397
Qy	2478 TTGGGCGCTTTTCGGTTTCCTCGCTCACTGATCGCTCGCTCGGTCGGTTCGGTTCGGC 2537
Db	2396 TTGGGCGCTTTTCGGTTTCCTCGCTCACTGACTCGCTCGCTCGGTCGGTTCGGTTCGGC 2337
Qy	2538 GAGCGGTATCAGCTCACTCAAAGCGGTAATACGGTTATCCACAGAATCAGGGGATAACG 2597
Db	2336 GAGCGGTATCAGCTCACTCAAAGCGGTAATACGGTTATCCACAGAATCAGGGGATAACG 2277
Qy	2598 CAGGAAAGAACATGTGAGCAAAAGCCAGCAAAAGGCGAGGACCGTAAAGAGCCCGCT 2657
Db	2276 CAGGAAAGAACATGTGAGCAAAAGCCAGCAAAAGGCGAGGACCGTAAAGAGCCCGCT 2217
Qy	2658 TGCTGGCGTTTTTCCATAGGCTCGCCCCCTGTACGAGCATCAAAAAATCGACGCTCAA 2717
Db	2216 TGCTGGCGTTTTTCCATAGGCTCGCCCCCTGTACGAGCATCAAAAAATCGACGCTCAA 2157
Qy	2718 GTCAGAGTCGGGAAACCCGACAGGACTAATAGATACAGGCGGTTTCCCGCTGGAGCT 2777
Db	2156 GTCAGAGTCGGGAAACCCGACAGGACTAATAGATACAGGCGGTTTCCCGCTGGAGCT 2097
Qy	2778 CCCTCGTGCCTCTCTCTGTTCGACACCTGCGCTTACCGGATACCTGTCCGCGCTTCTCC 2837
Db	2096 CCCTCGTGCCTCTCTCTGTTCGACACCTGCGCTTACCGGATACCTGTCCGCGCTTCTCC 2037
Qy	2838 CTTCCGGAAGCGTGGCGCTTCTCAATGCTCAAGCTGTAGGTACTCAGTTTCGTTGAGG 2897
Db	2036 CTTCCGGAAGCGTGGCGCTTCTCAATGCTCAAGCTGTAGGTACTCAGTTTCGTTGAGG 1977
Qy	2898 TCGTTCCGCTCCAGCTGGGCTGTGTGACGAAACCCCGCTTCAGCCGAGCGCTGGCGCT 2957
Db	1976 TCGTTCCGCTCCAGCTGGGCTGTGTGACGAAACCCCGCTTCAGCCGAGCGCTGGCGCT 1917
Qy	2958 TATCCGGTAACATATCGTCTTGAGTCCAAACCGGTAAAGACACGACTTATCGCCACTGGCAG 3017
Db	1916 TATCCGGTAACATATCGTCTTGAGTCCAAACCGGTAAAGACACGACTTATCGCCACTGGCAG 1857
Qy	3018 CAGCACTGGTAAACAGGATTAGCAGAGGAGTATGTAGCGGCTGTACAGAGTTCTTTGA 3077
Db	1856 CAGCACTGGTAAACAGGATTAGCAGAGGAGTATGTAGCGGCTGTACAGAGTTCTTTGA 1797

```
Db 716 TTCAATCAGGCAACCGGATCGGCTTTGACAAAAGAACCGGGCCCTCGCTGA 657
Qy 4161 CAGCGGAACACGGGATCAGAGCAGCCGATGCTGTGTGCGCCAGTCATAGCCGAA 4220
Db 656 CAGCGGAACACGGGATCAGAGCAGCCGATGCTGTGTGCGCCAGTCATAGCCGAA 597
Qy 4221 TAGCCTCTCCACCCAAAGCGGCGGAGAACCTGCGTGCAATCCATCTTGTCAATCATCG 4280
Db 596 TAGCCTCTCCACCCAAAGCGGCGGAGAACCTGCGTGCAATCCATCTTGTCAATCATCG 537
Qy 4281 AAACATCCTCATCTCTCTTGTGATCAGAGCTTGATCCCTGCGCCATCAG 4332
Db 536 AAACATCCTCATCTCTCTTGTGATCAGAGCTTGATCCCTGCGCCATCAG 485

RESULT 12
BD063789 3600 bp DNA linear PAR 27-AUG-2002
LOCUS Insulin-like growth factor I (IGF)-1 expression system and methods
DEFINITION of use.
ACCESSION BD063789
VERSION BD063789.1 GI:22609392
KEYWORDS JP 2001505435-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 3600)
AUTHORS Coleman, M.; Schwartz, R. and Demayo, F. J.
TITILE Insulin-like growth factor I (IGF)-1 expression system and methods
of

JOURNAL Patent: JP 2001505435-A 2 24-APR-2001;
COMMENT BARENTIS INC. BAYLOR COLLEGE OF MEDICINE
PN JP 2001505435-A/2
PD 24-APR-2001
PF 01-DEC-1997 JP 1998525696
PR 02-DEC-1996 US 60/031539, 19-NOV-1997 US 08/974572 PI
MICHAEL COLEMAN, ROBERT SCHWARTZ, FRANCESCO J DEMAYO PC
C12N15/85, C07K14/65, A61K48/00, A01K67/027
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES
source
1..3600
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 39.7%; Score 1719; DB 6; Length 3600;
Best Local Similarity 90.8%; Pred. No. 0;
Matches 1923; Conservative 0; Mismatches 5; Indels 191; Gaps 1;

Qy 2214 CCAGCTTTTGTCCCTTTAGTGGGTTAATTCGAGCTTGGGTAATCATGCTCATAGC 2273
Db 20 CCAGCTTTTGTCCCTTTAGTGGGTTAATTCGAGCTTGGGTAATCATGCTCATAGC 79
Qy 2274 TGTTCCTGTGAAATTTGTATCCGCTCACAAATCCACAAACATACGAGCGGGAAGCA 2333
Db 80 TGTTCCTGTGAAATTTGTATCCGCTCACAAATCCACAAACATACGAGCGGGAAGCA 139
Qy 2334 TAAAGTGAAGCTGGGTCCTTAATGAGTGAGCTAACTCACATTAATTTGGTTCCGCT 2393
Db 140 TAAAGTGAAGCTGGGTCCTTAATGAGTGAGCTAACTCACATTAATTTGGTTCCGCT 199
Qy 2394 CACTGCCGCTTTCCAGTCGGGAAACCTGTCGTCGAGCTGCATTAATGAATCGGCCAAC 2453
Db 200 CACTGCCGCTTTCCAGTCGGGAAACCTGTCGTCGAGCTGCATTAATGAATCGGCCAAC 259
Qy 2454 GCSCGGGAGAGCGGTTTTCGTAATTTGGCGCTCTTTCCGCTTCCTCGCTCACTGACTCGC 2513
Db 260 GCSCGGGAGAGCGGTTTTCGTAATTTGGCGCTCTTTCCGCTTCCTCGCTCACTGACTCGC 319
```

```
Qy 2514 TGCCTCGTTCGTTCCGCTGCGGCGAGGGGTATCAGCTCACTCAAGCGCGTAATACGGT 2573
Db 320 TGCCTCGTTCGTTCCGCTGCGGCGAGGGGTATCAGCTCACTCAAGCGCGTAATACGGT 379
Qy 2574 TATCCACAGAAATCAGGGGATAACCGCAGAAAGAAATGTGTAGCAAAAGAGCGGCAGCAAAAGG 2633
Db 380 TATCCACAGAAATCAGGGGATAACCGCAGAAAGAAATGTGTAGCAAAAGAGCGGCAGCAAAAGG 439
Qy 2634 CCAGAAACCGTAAAGGCGCGTGTGTGCGTTTTTTCATAGGCTCGGCCCTCTGACG 2693
Db 440 CCAGAAACCGTAAAGGCGCGTGTGTGCGTTTTTTCATAGGCTCGGCCCTCTGACG 499
Qy 2694 AGCATCAAAAATCGACGCTCAAGTCAGAGGTGCGGAAACCCGACAGACTATAAAGAT 2753
Db 500 AGCATCAAAAATCGACGCTCAAGTCAGAGGTGCGGAAACCCGACAGACTATAAAGAT 559
Qy 2754 ACCAGGCGTTTCCCGCTGGAAGCTCCCTCGTGCCTCTCTCTGTTCCGACCCCTGCCGCTTA 2813
Db 560 ACCAGGCGTTTCCCGCTGGAAGCTCCCTCGTGCCTCTCTCTGTTCCGACCCCTGCCGCTTA 619
Qy 2814 CCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAAGCGTGGCGTTTCTCAATGCTCACGCT 2873
Db 620 CCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAAGCGTGGCGTTTCTCAATGCTCACGCT 679
Qy 2874 GTAGGTATCTCAGTTCCGCTGAGGTTCGCTCCAAAGCTGGCTGTGTGACAGAACCC 2933
Db 680 GTAGGTATCTCAGTTCCGCTGAGGTTCGCTCCAAAGCTGGCTGTGTGACAGAACCC 739
Qy 2934 CGTTTCAGCCCGACCGCTGCGCTTATCCGGTAACATATCGTCTTGAGTCCAAACCGGTAA 2993
Db 740 CGTTTCAGCCCGACCGCTGCGCTTATCCGGTAACATATCGTCTTGAGTCCAAACCGGTAA 799
Qy 2994 GACAGCACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGTATG 3053
Db 800 GACAGCACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGTATG 859
Qy 3054 TAGGCGGTGCTACAGAGTTCTTGAAGTGTGCTGCTTAACTACCGCTTACACTAGAAGACAG 3113
Db 860 TAGGCGGTGCTACAGAGTTCTTGAAGTGTGCTGCTTAACTACCGCTTACACTAGAAGACAG 919
Qy 3114 TATTTGGTATCTGCGCTCTGCTGAAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTT 3173
Db 920 TATTTGGTATCTGCGCTCTGCTGAAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTT 979
Qy 3174 GATCGGCAAAACAAACCCGCTGCTGAGGTGGTTTTTTTGTTCGAGCAGCAGATTA 3233
Db 980 GATCGGCAAAACAAACCCGCTGCTGAGGTGGTTTTTTTGTTCGAGCAGCAGATTA 1039
Qy 3234 CCGCAGAAAAAAGGATCTCAAGAGATCTCTTGATCTTTTCTAGCGGTCTGACGCTC 3293
Db 1040 CCGCAGAAAAAAGGATCTCAAGAGATCTCTTGATCTTTTCTAGCGGTCTGACGCTC 1097
Qy 3294 AGTGGAAACGAAACCTCACGTTAAGGATTTTGGTCTATGACGGATACATATTTGAATGTA 3353
Db 1098 ----- 1097
Qy 3354 TTTAGAAAAATAACAAATAGGGTTTCGCGCACATTTCCCGAAAAAGTGCCACCTGTAT 3413
Db 1098 ----- 1097
Qy 3414 GCGGTGTGAATAACCGCACAGATGCTAAGGAGAAAAATACCGCATCAGGAAATTTGAAGC 3473
Db 1098 ----- 1097
Qy 3474 GTTAAATTAATTCAGAGAACTCGTCAAGAAAGGCGATAGAGGGGATCGGCTGCGAATCGGG 3533
Db 1098 -----TCAGAGAACTCGTCAAGAAAGGCGATAGAGGGGATCGGCTGCGAATCGGG 1148
Qy 3534 AGCGGCGATACCGTAAAGCAACGAGGAAGCGGTTCAGCCCATTCGCCCCAAAGCTCTTCAGC 3593
Db 1149 AGCGGCGATACCGTAAAGCAACGAGGAAGCGGTTCAGCCCATTCGCCCCAAAGCTCTTCAGC 1208
Qy 3594 AATATCACGGGTAGCCAAACGCTATGTCTCTGATAGCGGTTCGCCACACCCAGCGGCAACA 3653
```

Db 1209 AATATCAGGGTAGCCAAACGATATCTCTGATAGCGTCCGCCACACCCAGCGGCCACA 1268
Qy 3654 GTCCATGAATCCAGAAAGCGGCCATTTCCACCATGATATTCGGCAAGCAGGCATCGCC 3713
Db 1269 GTCATGAATCCAGAAAGCGGCCATTTCCACCATGATATTCGGCAAGCAGGCATCGCC 1328
Qy 3714 ATGGGTCAACGACGAGATCCTCGCGTCGGGTCATGCTCGCCCTTGAGCCTGGCGAACAGTTC 3773
Db 1329 ATGGGTCAACGACGAGATCCTCGCGTCGGGTCATGCTCGCCCTTGAGCCTGGCGAACAGTTC 1388
Qy 3774 GCTTGGCGGAGCCCTGATGCTCTTCGTCAGATCATCTGATCGACAGACCGGCTTC 3833
Db 1389 GGCTGGGCGGAGCCCTGATGCTCTTCGTCAGATCATCTGATCGACAGACCGGCTTC 1448
Qy 3834 CATCCGAGTAGCTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTTCGAATCGGCAGGTAGC 3893
Db 1449 CATCCGAGTAGCTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTTCGAATCGGCAGGTAGC 1508
Qy 3894 CGGATCAAGCGTATGACGCGCCGCTTGCATCAGCCATGATGATATCTTTCGCGCAGG 3953
Db 1509 CGGATCAAGCGTATGACGCGCCGCTTGCATCAGCCATGATGATATCTTTCGCGCAGG 1568
Qy 3954 AGCAAGTGAGATGACAGGAGATCCTGCGCCGCGCACTTCGCCCAATAGCAGCGATCCCT 4013
Db 1569 AGCAAGTGAGATGACAGGAGATCCTGCGCCGCGCACTTCGCCCAATAGCAGCGATCCCT 1628
Qy 4014 TCCCGCTTCAGTGACAGAGATGCGAGCAGCTGCGCAAGGACCGCCGTCGCGCAGCCA 4073
Db 1629 TCCCGCTTCAGTGACAGAGATGCGAGCAGCTGCGCAAGGACCGCCGTCGCGCAGCCA 1688
Qy 4074 CGATAGCGCGCTCGCTCGCTTTCAGTTCATTCAGGGGACCGGACAGGTCTTTCGAC 4133
Db 1689 CGATAGCGCGCTCGCTCGCTTTCAGTTCATTCAGGGGACCGGACAGGTCTTTCGAC 1748
Qy 4134 AAAAAGAACCGGGCGCCCTGCGCTGACAGCGGAAACAGCGGCGATCAGAGCAGCGCAT 4193
Db 1749 AAAAAGAACCGGGCGCCCTGCGCTGACAGCGGAAACAGCGGCGATCAGAGCAGCGCAT 1808
Qy 4194 TGTCTGTGTCGCCAGTCATAGCGGAATAGCTCTCCACCCCAAGCGGCGGAACTTCG 4253
Db 1809 TGTCTGTGTCGCCAGTCATAGCGGAATAGCTCTCCACCCCAAGCGGCGGAACTTCG 1868
Qy 4254 GTCAATCCATCTTGTTCATATCATGCGAAACGATCTCATCTCTCTCTTTCATCAGAGCT 4313
Db 1869 GTCAATCCATCTTGTTCATATCATGCGGAACGATCTCATCTCTCTCTTTCATCAGATCT 1928
Qy 4314 TGATCCCTCGGCCATCAG 4332
Db 1929 TGATCCCTCGGCCATCAG 1947

RESULT 13
BD069040
LOCUS
DEFINITION Treatment for urinary incontinence using gene therapy techniques.
ACCESSION BD069040
VERSION BD069040.1 GI:22614643
KEYWORDS JP 2001511154-A/2.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 3600)
AUTHORS Coleman, M.
TITLE Treatment for urinary incontinence using gene therapy techniques
JOURNAL Patent: JP 2001511154-A 2 07-AUG-2001;
COMMENT BARENTIS INC
OS Unidentified
PN JP 2001511154-A/2
PD 07-AUG-2001
PF 04-FEB-1998 JP 1998533206
PR 04-FEB-1997 US 60/038862
PI MICHAEL COLEMAN

PC A61K48/00
CC Strandedness: Single;
CC Topology: Linear;
CC Treatment for urinary incontinence using gene therapy CC
FH techniques
FT key Location/Qualifiers
FT source 1..3600
FT /organism='Unidentified'.
FEATURES
source Location/Qualifiers
1..3600
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
ORIGIN
Query Match 39.7%; Score 1719; DB 6; Length 3600;
Best Local Similarity 90.8%; Pred. No. 0;
Matches 1923; Conservative 0; Mismatches 5; Indels 191; Gaps 1;
Qy 2214 CCAGCTTTTGTTCCTTTAGTGGAGGTTAATTTTCGAGCTTGGCGTAAATCATGTGTCATAGC 2273
Db 20 CCAGCTTTTGTTCCTTTAGTGGAGGTTAATTTTCGAGCTTGGCGTAAATCATGTGTCATAGC 79
Qy 2274 TGTTCCTGTGTGAATTTGTATCCGCTCAAAATTCACAAACATACGAGCCGGAAGCA 2333
Db 80 TGTTCCTGTGTGAATTTGTATCCGCTCAAAATTCACAAACATACGAGCCGGAAGCA 139
Qy 2334 TAAAGTGTAAGGCTGGGCTGCTATGATGAGTAACTCACAATTAATTTGGCTTGGCT 2393
Db 140 TAAAGTGTAAGGCTGGGCTGCTATGATGAGTAACTCACAATTAATTTGGCTTGGCT 199
Qy 2394 CACTGCCCGCTTTCCAGTCGGGAAACCTGTGTCGCCAGCTGCAATTAATGAATCGGCCAAC 2453
Db 200 CACTGCCCGCTTTCCAGTCGGGAAACCTGTGTCGCCAGCTGCAATTAATGAATCGGCCAAC 259
Qy 2454 GCGCGGGAGAGCGGTTTGGCGTATTTGGCGCTCTTCCGCTTCTCGCTCACTGACTCGC 2513
Db 260 GCGCGGGAGAGCGGTTTGGCGTATTTGGCGCTCTTCCGCTTCTCGCTCACTGACTCGC 319
Qy 2514 TCGGCTCGGTCGTTCCGCTGCGGAGCGGTATCAGCTCACTCAAAAGGCGGTAAATAGCT 2573
Db 320 TCGGCTCGGTCGTTCCGCTGCGGAGCGGTATCAGCTCACTCAAAAGGCGGTAAATAGCT 379
Qy 2574 TATCCACAGAAATCAGGGGATTAACGAGGAAAGAAACATGTGAGCAAAAGGCCAGCAAAAGG 2633
Db 380 TATCCACAGAAATCAGGGGATTAACGAGGAAAGAAACATGTGAGCAAAAGGCCAGCAAAAGG 439
Qy 2634 CCAGGAAACCGTAAAAAGCGCGTTCGTCGGCGTTTTTTCATAGGCTCCGCCCCCTGACG 2693
Db 440 CCAGGAAACCGTAAAAAGCGCGTTCGTCGGCGTTTTTTCATAGGCTCCGCCCCCTGACG 499
Qy 2694 AGCATCACAATAATCCAGCTCAAGTCAGAGGTGGCGAAACCCGACGAGACTATAAGAT 2753
Db 500 AGCATCACAATAATCCAGCTCAAGTCAGAGGTGGCGAAACCCGACGAGACTATAAGAT 559
Qy 2754 ACCAGCGTTTCCCTCCCTGGAAGCTCCCTGCGGCTCTCTGTCGAGCCCTCCCGCTTA 2813
Db 560 ACCAGCGTTTCCCTCCCTGGAAGCTCCCTGCGGCTCTCTGTCGAGCCCTCCCGCTTA 619
Qy 2814 CCGGATACCTGTCCGCTTTTCCCTTCGGGAAGCGTGGCGCTTTCATATGCTCAGCT 2873
Db 620 CCGGATACCTGTCCGCTTTTCCCTTCGGGAAGCGTGGCGCTTTCATATGCTCAGCT 679
Qy 2874 GTAGGTATCTCAGTTGCTAGTGTGCTGCTCCAGCTGCGCTGTGTGTCAGCAAGACCCC 2933
Db 680 GTAGGTATCTCAGTTGCTAGTGTGCTGCTCCAGCTGCGCTGTGTGTCAGCAAGACCCC 739
Qy 2934 CCGTTCCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGTAGTCAACCCCGTAA 2993
Db 740 CCGTTCCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGTAGTCAACCCCGTAA 799
Qy 2994 GACACGATATCGCCACTGGCGAGCGCACTCGGTAAACAGGATTAGCAGAGCGAGGTATG 3053
Db 740 CCGTTCCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGTAGTCAACCCCGTAA 799

Db	800	GACACGACTTATCGCCCACTGGCGACGACCACTGGTAA CAGGATTTAGCAGGCGAGGTATG	859
Qy	3054	TAGCGCGTGCTACAGAGTTCTTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGGACAG	3113
Db	860	TAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGGACAG	919
Qy	3114	TATTTGGTATCTCGGCTCTGCTGAAGCCAGTTTACCTTCGGAANAAGAGTTGTTAGCTCTT	3173
Db	920	TATTTGGTATCTCGGCTCTGCTGAAGCCAGTTTACCTTCGGAANAAGAGTTGTTAGCTCTT	979
Qy	3174	GATTCGGCAAAACAAACACCGCTGTGTAGCGGTGTTTTTTTGTTCGAAGCAGCAGATTA	3233
Db	980	GATTCGGCAAAACAAACCGCTGTGTAGCGGTGTTTTTTTGTTCGAAGCAGCAGATTA	1039
Qy	3234	CGCGCAGAAAAAAGAGTCTCAAGAAAGATCTCTTTTGATCTTTTCTACGGGGTCTGACGCTC	3293
Db	1040	CGCGCAGAAAAAAGAGTCTCAAGAAAGATCTCTTTTGATCTTTTCTACGGGGTCTGACG--	1097
Qy	3294	AGTGGACGAAACTCACGTTAAGGATTTTGCTCATGAGCGGATACATATTTGAATGTA	3355
Db	1098	-----	1097
Qy	3354	TTTAGAAAAATAAACAAATAGGGTTTCGCGCA CATTTCCCGAAAAGTGCCACCTGTAT	3413
Db	1098	-----	1097
Qy	3414	CGCGTGAATACCGGCACAGATCGGTAGGAGAAATACC GCATCAGGAAATGTTAAGC	3473
Db	1098	-----	1097
Qy	3474	GTTAATAATT CAGAAGAACTCGTCAAGAAAGCGATAGAAAGCGATCGCTGCGAATCGGG	3533
Db	1098	-----TCAGNAGAACTCGTCAAGAAAGCGATAGAAAGCGATCGCTGCGAATCGGG	1148
Qy	3534	AGCGCGATACCGTAAAGCACAGGAAAGCGGT CAGCCCATTCGCCGCCAAGCTCTTTCAGC	3593
Db	1149	AGCGCGCATACCGTAAAGCACAGGAAAGCGGT CAGCCCATTCGCCGCCAAGCTCTTTCAGC	1208
Qy	3594	AATATCAGGGTAGCCCAACGCTATGCTCATAGCGGTCCGCCACACCCAGCCGCGGCACA	3653
Db	1209	AATATCAGGGTAGCCCAACGCTATGCTCATAGCGGTCCGCCACACCCAGCCGCGGCACA	1268
Qy	3654	GTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGAAGCAGGCAATCGCC	3713
Db	1269	GTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGAAGCAGGCAATCGCC	1328
Qy	3714	ATGGGT CACGACAGAGTCTCGCGT CGGGCATGCTCGCCTCAGCTCGCGCATCGCAACAGTTTC	3773
Db	1329	ATGGGT CACGACAGAGTCTCGCGT CGGGCATGCTCGCCTCAGCTCGCGCATCGCAACAGTTTC	1388
Qy	3774	GGCTGGCGCAGCCCTCGATGCTCTTCGTCAGATCATCTCTGATCGCAAGACCGGCTTC	3833
Db	1389	GGCTGGCGCAGCCCTCGATGCTCTTCGTCAGATCATCTCTGATCGCAAGACCGGCTTC	1448
Qy	3834	CATCGAGTAGCTGCTCGCTCGATGCGATGTTTCGCTTGTGTGTCGATCGAATGGGCAGGTAGC	3893
Db	1449	CATCGAGTAGCTGCTCGCTCGATGCGATGTTTCGCTTGTGTGTCGATCGAATGGGCAGGTAGC	1508
Qy	3894	CGGATCAAGCGTATGACGCCGCCCATTTGCATCAGCCATGATGATACTTTCTCGGCAGG	3953
Db	1509	CGGATCAAGCGTATGACGCCGCCCATTTGCATCAGCCATGATGATACTTTCTCGGCAGG	1568
Qy	3954	AGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCGCCCAATAGCAGCCAGTCCCT	4013
Db	1569	AGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCGCCCAATAGCAGCCAGTCCCT	1628
Qy	4014	TCCCGCTTCAGTGACAACGTCGACAGCATGTCGCAAGGAACGCCCTGCTGGCCAGCCCA	4073
Db	1629	TCCCGCTTCAGTGACAACGTCGACAGCATGTCGCAAGGAACGCCCTGCTGGCCAGCCCA	1688
Qy	4074	CGATAGCCGCTGCTCCGTTTGAGGTTCAATTCAGGGCACCGGACAGGTCTTGTC	4133
Db	1689	CGATAGCCGCTGCTCCGTTTGAGGTTCAATTCAGGGCACCGGACAGGTCTTGTC	1748

Qy	4134	AAAAAGAACGGGCGCCCTTGCCTCACAGCCGGACACGGCGGCATCAGAGCAGCCGAT	4193
Db	1749	AAAAAGAACGGGCGCCCTTGCCTCACAGCCGGAAACGGCGGCATCAGAGCAGCCGAT	1808
Qy	4194	TGTCCTGTTGTGCCAGTCATAGCCGAATAGCCTCTCCACCAGCGCGCGAACAACCTGC	4253
Db	1809	TGTCCTGTTGTGCCAGTCATAGCCGAATAGCCTCTCCACCAGCGCGCGAACAACCTGC	1868
Qy	4254	GTCGAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCTCTCTTGATCAGAGCT	4313
Db	1869	GTCGAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCTCTCTTGATCAGATCT	1928
Qy	4314	TGATCCCTCGGCCATCAG	4332
Db	1929	TGATCCCTCGGCCATCAG	1947
<hr/>			
RESULT 14			
BD136049		3426 bp DNA linear	PAT 18-SEP-2002
LOCUS			
DEFINITION		Interferon alpha plasmid and delivery system and method of preparing and using the same.	
ACCESSION		BD136049	
VERSION		BD136049.1 GI:23230994	
KEYWORDS		JP 2002506647-A/16.	
SOURCE		synthetic construct	
ORGANISM		other sequences; artificial sequences.	
REFERENCE		1 (bases 1 to 3426)	
AUTHORS		Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.	
TITLE		Interferon alpha plasmid and delivery system and method of preparing and using the same	
JOURNAL		Patent: JP 2002506647-A 16 05-MAR-2002;	
COMMENT		VALENTIS INC	
		OS Artificial Sequence	
		PN JP 2002506647-A/16	
		PD 05-MAR-2002	
		PF 12-MAR-1999 JP 2000536861	
		PR 19-MAR-1998 US 60/078654	
		PI JEFF NORDSTROM, FEDERICA PERICLE, ALAIN ROLLAND, ROBERT RALSTON	
		PC C12N15/09, A61K38/21, A61K48/00, A61P35/00, C07K14/54, C07K14/56,	
		PC C12N1/15,	
		PC C12N1/19, C12N1/21, C12N5/10//A61K9/127, C12N15/00, A61K37/66, PC C12N5/00	
		CC Sequence source: synthetic construct	
		FH Key Location/Qualifiers	
		FT source 1..3426	
		PT Location/Qualifiers	
FEATURES		1..3426	
source		/organism="synthetic construct"	
		/mol_type="genomic DNA"	
		/db_xref="taxon:32630"	
<hr/>			
ORIGIN			
Query Match 39.7%; Score 1718.4; DB 6; Length 3426;			
Best Local Similarity 90.5%; Pred. No. 0;			
Matches 1926; Conservative 11; Indels 191; Gaps 1			
<hr/>			
Qy	2205	GCCACAGCTCCAGCTTTTGTTCCTTTAGTAGGAGGTTAAATTTCGAGCTTGGCGTAATCAT	2266
Db	793	GGCCCGGTACACAGCTTTTGTTCCTTTAGTAGGAGGTTAAATTTCGAGCTTGGCGTAATCAT	852
Qy	2265	GGTCATAGCTGTTCTGTGTGAATTTGTTCCTTCATCGCTCACAATTCACACATACGAG	2322
Db	853	GGTCATAGCTGTTCTGTGTGAATTTGTTCCTTCATCGCTCACAATTCACACATACGAG	912
Qy	2325	CGGGAAGCATAAAGTGTAAAGCTTGGGTGCTTAATGAGTGAGCTAACTCACTTAATTG	2388
Db	913	CCGGAAGCATAAAGTGTAAAGCTTGGGTGCTTAATGAGTGAGCTAACTCACTTAATTG	972
Qy	2385	CGTTGGCTACTACTGCCCGCTTTCCAGTCGGGAAAACCTGTGTCGAGCTGCATTAATGNA	2444

JOURNAL	Patent: WO 2004067719-A 11 12-AUG-2004;
Advisys, Inc. (US)	
Location/Qualifiers	
source	1. .3534
FEATURES	/organism="synthetic construct"
	/mol_type="unassigned DNA"
	/db_xref="taxon:32630"
	/note="This is the nucleic acid sequence for the
	operatively linked comp onents of the HV-GHRH plasmid."
ORIGIN	
QY	2205 GCCACAGCTCCAGCTTTTGTCCCTTTAGTGGAGGTTAATTCGAGCTTGGCGTAATCAT 2264
Db	1366 GGCCCGGTACAGCTTTTGTTCCTTTAGTGGAGGTTAATTCGAGCTTGGCGTAATCAT 1425
QY	2265 GGTATAGTCTGTTCCCTGTGTGAATTTCTATCCGCTCACAAATCCACAAACATACGAG 2324
Db	1426 GGTATAGTCTGTTCCCTGTGTGAATTTCTATCCGCTCACAAATCCACAAACATACGAG 1485
QY	2325 CCGAAGCATAAAGTGTAAAGCTGGGTGCTTAATGAGTGAGCTAACTACATTAATTG 2384
Db	1486 CGGAAGCATAAAGTGTAAAGCTGGGTGCTTAATGAGTGAGCTAACTACATTAATTG 1545
QY	2385 GTTTGGCTCTACTGCCGCTTTCAGTCCGGGAAACCTGCTGCGAGCTGCATTAATGAA 2444
Db	1546 GTTTGGCTCTACTGCCGCTTTCAGTCCGGGAAACCTGCTGCGAGCTGCATTAATGAA 1605
QY	2445 TCGGCCAAACCGCGGGAGAGCGGTTTGGCTATTGGCGCTCTTCCGCTTCCCTCGCTCA 2504
Db	1606 TCGGCCAAACCGCGGGAGAGCGGTTTGGCTATTGGCGCTCTTCCGCTTCCCTCGCTCA 1665
QY	2505 CTGACTCGCTGCGTTCGCTGCTGCGGAGAGCGGTTTGGCTATTGGCGCTCTTCCGCTTCCCTCGCTCA 2564
Db	1666 CTGACTCGCTGCGTTCGCTGCTGCGGAGAGCGGTTTGGCTATTGGCGCTCTTCCGCTTCCCTCGCTCA 1725
QY	2565 TAATACGGTTATCCACAGATCAGGGGATACGAGGAAAGAAATGAGCAAAAGGCC 2624
Db	1726 TAATACGGTTATCCACAGATCAGGGGATACGAGGAAAGAAATGAGCAAAAGGCC 1785
QY	2625 AGCAAAAGCCAGGAAACCGTAAAGAGCGGTTTGGCTGCGGTTTTCATAGGCTCCGCC 2684
Db	1786 AGCAAAAGCCAGGAAACCGTAAAGAGCGGTTTGGCTGCGGTTTTCATAGGCTCCGCC 1845
QY	2685 CCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGTGGCGAAACCGCAGGAC 2744
Db	1846 CCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGTGGCGAAACCGCAGGAC 1905
QY	2745 TATAAAGATACAGAGGTTTCCCTCGGAAGCTCCCTGCGCTCTCTGTTCCGAGCC 2804
Db	1906 TATAAAGATACAGAGGTTTCCCTCGGAAGCTCCCTGCGCTCTCTGTTCCGAGCC 1965
QY	2805 TGCCGCTTACCGGATACCTGTCGCGCTTTCCTCTTCCGGAAGCGTGGCGTTTCTCAAT 2864
Db	1966 TGCCGCTTACCGGATACCTGTCGCGCTTTCCTCTTCCGGAAGCGTGGCGTTTCTCAAT 2025
QY	2865 GCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCCGCTTCCGAGCTGGGCTGTGC 2924
Db	2026 GCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCCGCTTCCGAGCTGGGCTGTGC 2085
QY	2925 ACGAACCCCGCTTACGCCGAGACCGCTGCGCTTATCCGGTAACTATCGTCTTGTAGTCCA 2984
Db	2086 ACGAACCCCGCTTACGCCGAGACCGCTGCGCTTATCCGGTAACTATCGTCTTGTAGTCCA 2145
QY	2985 ACCCGGTAAAGACGACTTATCCGCACTGGGAGAGCCCTCGGTAAACAGGATAGCAGAG 3044
Db	2146 ACCCGGTAAAGACGACTTATCCGCACTGGGAGAGCCCTCGGTAAACAGGATAGCAGAG 2205
QY	3045 CCAGGTATCTAGGCGGTGTACAGAGTCTTGAAGTGGTGGCTTAACCTACGCTACACTA 3104

Db	2206 CGAGGTATGTAGCGGTGCTTACAGAGTTCTTGAAGTGGTGGCCCTAACTACGCGCTACACTA 2265
QY	3105 GAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCAGGTTTACCTTCGGAAGAGAGTTG 3164
Db	2266 GAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCAGGTTTACCTTCGGAAGAGAGTTG 2325
QY	3165 GTAGCTTCTGATCCGCGCAAAACAAACCAACCGCTGCTGAGCGGTGTTTTTGTTCGAGC 3224
Db	2326 GTAGCTTCTGATCCGCGCAAAACAAACCAACCGCTGCTGAGCGGTGTTTTTGTTCGAGC 2385
QY	3225 AGCAGATTACGCGCAGGAAAGGATCTCAAGAGATCTTTTGTATCTTTTCTACGGGT 3284
Db	2386 AGCAGATTACGCGCAGGAAAGGATCTCAAGAGATCTTTTGTATCTTTTCTACGGGT 2445
QY	3285 CTGACGCTCAGTGGAAACGAAACTCACGTTAAGGGATTTTGGTCTATGAGCGGATACATAT 3344
Db	2446 CTGAGC----- 2452
QY	3345 TTGAATGATTGAAGAAATAACAAATAGGGTTCCGCGCACATTTCCCGGAAAGTGC 3404
Db	2453 ----- 2452
QY	3405 CACCTGTATCGGTGTGAATACCGCACAGATCGTAAAGGAGAAATACCGCATCAGGA 3464
Db	2453 ----- 2452
QY	3465 ATTGTAGCGTTAATAATTTCAGAAAGAACTCGTCAAGAGGCGATAGAGGCGATGCGGTG 3524
Db	2453 -----TCAGAAAGAACTCGTCAAGAGGCGATAGAGGCGATGCGGTG 2494
QY	3525 CGAATCGGGAGCGCGATACCGTAAAGCAACAGAGAGCGGTACGCCATTCGCGCCAG 3584
Db	2495 CGAATCGGGAGCGCGATACCGTAAAGCAACAGAGAGCGGTACGCCATTCGCGCCAG 2554
QY	3585 CTCTTCAGCAATATCACGGGTAGCCAAACGCTATGTCTGTATAGCGGTCCGCCACACCCAG 3644
Db	2555 CTCTTCAGCAATATCACGGGTAGCCAAACGCTATGTCTGTATAGCGGTCCGCCACACCCAG 2614
QY	3645 CCGGCCACAGTCGATGAATCCAGAAAGCGGCCATTTTCCACCATGATATTTCCGGCAAGCA 3704
Db	2615 CCGGCCACAGTCGATGAATCCAGAAAGCGGCCATTTTCCACCATGATATTTCCGGCAAGCA 2674
QY	3705 GGCATCGCATGCGGTTCACAGAGATCTCCGCTGCGGCGATGCTCGCTTTGAGCTGGC 3764
Db	2675 GGCATCGCATGCGGTTCACAGAGATCTCCGCTGCGGCGATGCTCGCTTTGAGCTGGC 2734
QY	3765 GAAACAGTTTCGCTGCGCGAGCCCTGATGCTCTTCGTCCAGATCATCTGTATCGACAG 3824
Db	2735 GAAACAGTTTCGCTGCGCGAGCCCTGATGCTCTTCGTCCAGATCATCTGTATCGACAG 2794
QY	3825 ACCGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCCAAATGG 3884
Db	2795 ACCGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCCAAATGG 2854
QY	3885 GCAGTACCGGATCAAGCGGTATGAGCGCGCATTCGATCGCATGATGATGATGATGATGAT 3944
Db	2855 GCAGTACCGGATCAAGCGGTATGAGCGCGCATTCGATCGCATGATGATGATGATGATGAT 2914
QY	3945 CTCCGACAGGAGCAAGGTGAGATGACAGGAGATCTCCCGCGGCACTTCGCCCAATAGCAG 4004
Db	2915 CTCCGACAGGAGCAAGGTGAGATGACAGGAGATCTCCCGCGGCACTTCGCCCAATAGCAG 2974
QY	4005 CAGTCCCTTCCGCTTCAAGTGAACAGTCCGAGCAGCTGCGCAAGGAGACCGCGTCT 4064
Db	2975 CAGTCCCTTCCGCTTCAAGTGAACAGTCCGAGCAGCTGCGCAAGGAGACCGCGTCTCT 3034
QY	4065 GSCCAGCCACGATAGCGCGTCTCGCTTCTGAGTTCATTCAGGGCACCCGACAGGTC 4124
Db	3035 GSCCAGCCACGATAGCGCGTCTCGCTTCTGAGTTCATTCAGGGCACCCGACAGGTC 3094
QY	4125 GGTCTTGACAAAGAAACCGGGCGCCCTGCGCTGACAGCGGAAACACGCGCGCATCAGA 4184
Db	3095 GGTCTTGACAAAGAAACCGGGCGCCCTGCGCTGACAGCGGAAACACGCGCGCATCAGA 3154

Qy	4185	GCAGCCGATTCTGTGTGCCCCAGTCATAGCCGAATAGCCTCTCCACCCCAAGCGCGG	4244
Db	3155	GCAGCCGATTCTGTGTGCCCCAGTCATAGCCGAATAGCCTCTCCACCCCAAGCGCGG	3214
Qy	4245	AGAACCTGCGTGCAATCCATCTTGTTCATCATGCGAAACGATCCTCATCCTGTCTCTTG	4304
Db	3215	AGAACCTGCGTGCAATCCATCTTGTTCATCATGCGAAACGATCCTCATCCTGTCTCTTG	3274
Qy	4305	ATCAGAGCTTCATCCCTGCGCCATCAG	4332
Db	3275	ATCAGATCTTGATCCCTGCGCCATCAG	3302

Search completed: March 16, 2006, 01:29:29
Job time : 20887 secs

This Page Blank (uspto)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2006, 19:30:36 ; Search time 2263 Seconds
(without alignments)

12758.042 Million cell updates/sec

Title: US-10-811-028A-1

Perfect score: 4331

Sequence: 1 cggcgccggcctcttcgcta.....ttgatccctgcgcacatcag 4332

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001as.*

5: Geneseq2001bs.*

6: Geneseq2002as.*

7: Geneseq2002bs.*

8: Geneseq2003as.*

9: Geneseq2003bs.*

10: Geneseq2003cs.*

11: Geneseq2003ds.*

12: Geneseq2004as.*

13: Geneseq2004bs.*

14: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4331	100.0	4332	13	Adt55135 Nucleotid
2	4170.6	96.3	4293	13	Adt55136 Nucleotid
3	3245.6	74.9	4187	13	Adt55140 Nucleotid
4	3147.8	72.7	4058	13	Adt55139 Nucleotid
5	2341.8	54.1	5753	13	Adt55137 Nucleotid
6	2341.8	54.1	5760	13	Adt55138 Nucleotid
7	1937	44.7	3609	5	Aai70085 Plasmid p
8	1924.4	44.4	3589	5	Aai70084 Plasmid p
9	1923.8	44.4	3589	2	Aaz40418 Plasmid p
10	1923.8	44.4	3589	12	Adf77242 Human IFN
11	1845.4	42.6	8349	3	Aaa15565 pMON30464
12	1844.4	42.6	11546	13	AdU73266
13	1719	39.7	3600	2	Aav50427 Plasmid p
14	1719	39.7	3600	2	Aav50427 Expected
15	1719	39.7	5707	2	Aax88055 Plasmid p
16	1718.4	39.7	2192	6	Abq78294 Nucleotid
17	1718.4	39.7	3026	10	Aad53819 pGHRH1674
18	1718.4	39.7	3426	2	Aaz40416 Plasmid p
19	1718.4	39.7	3426	12	Adf77240 Mouse int

20	1718.4	39.7	3534	6	ABQ78293
21	1718.4	39.7	3534	9	AAL62060
22	1718.4	39.7	3534	9	AAL62062
23	1718.4	39.7	3534	9	AAL62059
24	1718.4	39.7	3534	9	AAL62058
25	1718.4	39.7	3534	9	AAL62061
26	1718.4	39.7	3534	9	AAL62061
27	1718.4	39.7	3534	9	AAL60444
28	1718.4	39.7	3534	9	AAL60445
29	1718.4	39.7	3534	9	AAL60446
30	1718.4	39.7	3534	9	AAL60443
31	1718.4	39.7	3534	10	ACF04661
32	1718.4	39.7	3534	10	ACF04660
33	1718.4	39.7	3534	10	ACF04657
34	1718.4	39.7	3534	10	ACF04659
35	1718.4	39.7	3534	10	ACF04658
36	1718.4	39.7	3534	12	ADF90306
37	1718.4	39.7	3534	12	ADF90302
38	1718.4	39.7	3534	12	ADF90304
39	1718.4	39.7	3534	12	ADF90305
40	1718.4	39.7	3534	12	ADF90303
41	1718.4	39.7	3534	12	ADL70452
42	1718.4	39.7	3534	12	ADL70453
43	1718.4	39.7	3534	12	ADL70454
44	1718.4	39.7	3534	12	ADO31099
45	1718.4	39.7	3534	12	ADO31100

ALIGNMENTS

RESULT 1

ADT55135

ID ADT55135 standard; DNA; 4332 BP.

XX

AC ADT55135;

XX

DT 30-DEC-2004 (first entry)

XX

DE Nucleotide sequene of expression vector pMB1-MnSOD.

XX

KW Ophthalmological; radiation; free radical; superoxide anion;
KW heavy metal cation; metallothionein; superoxide dismutase; SOD; catalase;
KW glutathione peroxidase 4; GPx-4; gamma glutamyl transpeptidase;
KW xerostomia; xerophthalmia; autoimmune disorder; Sjogren's syndrome;
KW graft-versus-host disease; systemic lupus erythematosus;
KW rheumatoid arthritis; HIV-1 infection; ageing; autonomic dysfunction;
KW psychogenic disorder; trauma; hepatitis C; cancer; mastication; ss.

OS Homo sapiens.

OS Simian virus 40.

OS Synthetic.

XX

Key Location/Qualifiers

CDS 2..781

FT /*tag= a

FT /note= "human Manganese superoxide dismutase cDNA"

FT intron 312..497

FT /*tag= b

FT polyA_signal /note= "human beta-globin intron"

FT /tag= c

FT /note= "SV40 late gene polyadenylation signal"

FT promoter 471..1162

FT /*tag= d

FT /note= "CMV promoter"

FT rep_origin 1158..1825

FT /*tag= e

FT /note= "ColE1 ori from pBluescript SK+"

FT CDS 1236..2020

FT /*tag= f

FT /gene= "kanamycin resistance gene"

XX

1501 GCACCTGAAGTTCAATGGTGGTGCATATCAATCATAGCATTTTCTGGCAAAACCTCAGC 1560
1501 GCACCTGAAGTTCAATGGTGGTGCATATCAATCATAGCATTTTCTGGCAAAACCTCAGC 1560
1561 CCTAACCGGTGGAGAACCCAAAGGGAGTGTGGAAGCCATCAAACTGACTTTGGT 1620
1561 CCTAACCGGTGGAGAACCCAAAGGGAGTGTGGAAGCCATCAAACTGACTTTGGT 1620
1621 TCCTTTGACCAAGTTTAAAGGAGAGCTGACGGCTGCATCTGTTGGTCCAAAGGCTCAGGT 1680
1621 TCCTTTGACCAAGTTTAAAGGAGAGCTGACGGCTGCATCTGTTGGTCCAAAGGCTCAGGT 1680
1681 TGGGGTTGGCTTGGTTTCAATAAGGAACGGGACCTTACAAATTTGCTGTCCAAAT 1740
1681 TGGGGTTGGCTTGGTTTCAATAAGGAACGGGACCTTACAAATTTGCTGTCCAAAT 1740
1741 CAGGATCCACTGCAAGGAAACCAAGGCTTTATTCACCTGCTGGGGATTGATGTGGGAG 1800
1741 CAGGATCCACTGCAAGGAAACCAAGGCTTTATTCACCTGCTGGGGATTGATGTGGGAG 1800
1801 CAGGCTTACTACCTTCAGATATAAAGTCAAGGCTGATTTATTAAGGCTTATTTGGAAT 1860
1801 CAGGCTTACTACCTTCAGATATAAAGTCAAGGCTGATTTATTAAGGCTTATTTGGAAT 1860
1861 GTAATCAACTGGGGAGAAATGTAAGTCAAGGCTGATTTATTAAGGCTTATTTGGAAT 1920
1861 GTAATCAACTGGGGAGAAATGTAAGTCAAGGCTGATTTATTAAGGCTTATTTGGAAT 1920
1921 CGTTATGCTGGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1980
1921 CGTTATGCTGGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1980
1981 AAAAAACGGAAATCCCTGCAAGCCGGGGATCCACTAGTTCTAGAGCGCGCCACCGCG 2040
1981 AAAAAACGGAAATCCCTGCAAGCCGGGGATCCACTAGTTCTAGAGCGCGCCACCGCG 2040
2041 GTGAGCTCCCAACTAGAAATGCAAGTGAAGAAAAATGCTTTATTTGTGAATTTGTGATGC 2100
2041 GTGAGCTCCCAACTAGAAATGCAAGTGAAGAAAAATGCTTTATTTGTGAATTTGTGATGC 2100
2101 TATGCTTTATTTGTAACCAATTAAGCTGCAATAAACAAGTTAAACAATTTGCAATCA 2160
2101 TATGCTTTATTTGTAACCAATTAAGCTGCAATAAACAAGTTAAACAATTTGCAATCA 2160
2161 TTTTATGTTTCAGGTTCCAGGGGAGGTGGAGGTTTTTAAAGCCACAGCTCCAGCTT 2220
2161 TTTTATGTTTCAGGTTCCAGGGGAGGTGGAGGTTTTTAAAGCCACAGCTCCAGCTT 2220
2221 TTGTTCCCTTTAGTGAGGGTTAATTTCCAGCTTGGGGTAAATCATGTTGCTGTTTCC 2280
2221 TTGTTCCCTTTAGTGAGGGTTAATTTCCAGCTTGGGGTAAATCATGTTGCTGTTTCC 2280
2281 TGTGTAATTTGTTATCCGCTCACAATTCACACATACGAGCCGGAAGCAATAAGTG 2340
2281 TGTGTAATTTGTTATCCGCTCACAATTCACACATACGAGCCGGAAGCAATAAGTG 2340
2341 TAAAGCCTGGGGTCCCTAATGAGTGAGTAACTCACAATTAATGCTGCTCAGCTGCC 2400
2341 TAAAGCCTGGGGTCCCTAATGAGTGAGTAACTCACAATTAATGCTGCTCAGCTGCC 2400
2401 CGCTTTCCAGTCGGGAAACCTGCTGCTGCCAGTGCATTAATGAATCGGCCAAACGCGGG 2460
2401 CGCTTTCCAGTCGGGAAACCTGCTGCTGCCAGTGCATTAATGAATCGGCCAAACGCGGG 2460
2461 GAGAGGCGGTTTGGGATTTGGGCGCTTCCGCTTCCGCTCAGTCACTGCTGCGCTC 2520
2461 GAGAGGCGGTTTGGGATTTGGGCGCTTCCGCTTCCGCTCAGTCACTGCTGCGCTC 2520
2521 GGTGTTCCGCTGCGGCGAGCGGTATCAGGCTCACTCAAGGCGGTAATACGGTTATCCAC 2580
2521 GGTGTTCCGCTGCGGCGAGCGGTATCAGGCTCACTCAAGGCGGTAATACGGTTATCCAC 2580

2581 AGAATCAGGGATAACCGAGGAAGAACATGTGAGCAAAAGCCAGCAAAAGCCAGGAA 2640
2581 AGAATCAGGGATAACCGAGGAAGAACATGTGAGCAAAAGCCAGCAAAAGCCAGGAA 2640
2641 CCGTAAAAAGGCGCGCTTGTGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCA 2700
2641 CCGTAAAAAGGCGCGCTTGTGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCA 2700
2701 CAAAAATCCAGCGCTCAAGTCCAGAGTGGGGAACCCGACAGGACTATAAAGATACCAAGC 2760
2701 CAAAAATCCAGCGCTCAAGTCCAGAGTGGGGAACCCGACAGGACTATAAAGATACCAAGC 2760
2761 GTTTCGCCCTGGAGGCTCCCTCGTGGCTCTCTGTTCCGACCTCGCTTACCGGATA 2820
2761 GTTTCGCCCTGGAGGCTCCCTCGTGGCTCTCTGTTCCGACCTCGCTTACCGGATA 2820
2821 CCGTTCGCCCTTCTCCCTTCGGGAACGCTGGCGCTTTCTCAATGCTCAAGCTGTAGGTA 2880
2821 CCGTTCGCCCTTCTCCCTTCGGGAACGCTGGCGCTTTCTCAATGCTCAAGCTGTAGGTA 2880
2881 TCTCAGTTCGCTGCTAGTTCGCTCCAGCTGGGCTGTGTCAGCAAAACCCCGCTTCA 2940
2881 TCTCAGTTCGCTGCTAGTTCGCTCCAGCTGGGCTGTGTCAGCAAAACCCCGCTTCA 2940
2941 GCCCGACCGCTGCGCTTATCCGCTAACTATCGTCTTGAGTCCAAACCCCGCTTCA 3000
2941 GCCCGACCGCTGCGCTTATCCGCTAACTATCGTCTTGAGTCCAAACCCCGCTTCA 3000
3001 CTTTATGCCACTGGCAGCAGCCACTGCTAACAGGATTAGCAGAGGCTATGTAGCGG 3060
3001 CTTTATGCCACTGGCAGCAGCCACTGCTAACAGGATTAGCAGAGGCTATGTAGCGG 3060
3061 TGTCTACAGAGTTCCTCAAGTGGTGGCTAACTACGCTACACTAGAGGACAGTATTGG 3120
3061 TGTCTACAGAGTTCCTCAAGTGGTGGCTAACTACGCTACACTAGAGGACAGTATTGG 3120
3121 TATCTCGCTCTGCTGAAAGCCAGTTACCTTCGGAAGAGTTGGTAGTCTTGTATCCG 3180
3121 TATCTCGCTCTGCTGAAAGCCAGTTACCTTCGGAAGAGTTGGTAGTCTTGTATCCG 3180
3181 CAAACAAACCCGCTGGTAGCGGTGTTTTTTGTTTCCAGCAGCAGATTACGCGCAG 3240
3181 CAAACAAACCCGCTGGTAGCGGTGTTTTTTGTTTCCAGCAGCAGATTACGCGCAG 3240
3241 AAAAAAGGATCTCAAGAAAGATCCTTTGATCTTTCTACGGGCTCTGACGCTCAGTGGAA 3300
3241 AAAAAAGGATCTCAAGAAAGATCCTTTGATCTTTCTACGGGCTCTGACGCTCAGTGGAA 3300
3301 CGAAAACTCAAGTTAAGGGATTTTGGTTCATGAGCGGATACATATTTGAAATGTATTAGAA 3360
3301 CGAAAACTCAAGTTAAGGGATTTTGGTTCATGAGCGGATACATATTTGAAATGTATTAGAA 3360
3361 AATAAACAAATAGGGTTCCGCGCACATTTCCCGAAAGTCCCACTGTATGCGGTGT 3420
3361 AATAAACAAATAGGGTTCCGCGCACATTTCCCGAAAGTCCCACTGTATGCGGTGT 3420
3421 GAAATACCGCACAGATGCGTAAGGAGAAATACCGCATCAGGAAATTTGTAAGCGTTAATA 3480
3421 GAAATACCGCACAGATGCGTAAGGAGAAATACCGCATCAGGAAATTTGTAAGCGTTAATA 3480
3481 ATTCCAGAAACCTGCTCAAGAGCGGATAGAGCGGATGCGCTGCGAATCGGAGCGCGG 3540
3481 ATTCCAGAAACCTGCTCAAGAGCGGATAGAGCGGATGCGCTGCGAATCGGAGCGCGG 3540
3541 ATACCGTAAAGCACAGGAGCGGTCAGGCCATTTCCCGCAAGCTCTTCCAGCAATATCA 3600
3541 ATACCGTAAAGCACAGGAGCGGTCAGGCCATTTCCCGCAAGCTCTTCCAGCAATATCA 3600
3601 CCGGTAGCCAAACGCTATGCTGATAGCGGTCGCGCACACCCAGCGCGGCACAGTCGATG 3660
3601 CCGGTAGCCAAACGCTATGCTGATAGCGGTCGCGCACACCCAGCGCGGCACAGTCGATG 3660
3661 AATCCAGAAAGCGGCGCATTTTCCACCATGATATTCCGCAAGCAGGCGATCGCCATGGGTC 3720

|||||
3661 AATCAGAAAAGCGCCATTTTCCACCATGATATTCCGCAAGCAGGCATGCCATGGGTC 3720
QY
3721 ACGACGAGATCCTCGCGTGGGATGCTCGCCCTTGAGCCTGGGAAACAGTTCCGCTGGC 3780
Db
3721 ACGACGAGATCCTCGCGTGGGATGCTCGCCCTTGAGCCTGGGAAACAGTTCCGCTGGC 3780
QY
3781 CGGAGCCCTGATGCTCTTCTGTCAGATCATCTCTGATCGACAAGACCGGCTTCCATCCGA 3840
Db
3781 CGGAGCCCTGATGCTCTTCTGTCAGATCATCTCTGATCGACAAGACCGGCTTCCATCCGA 3840
QY
3841 GTACGTGCTCGTCGATCGATGTTTCGCTGGTGGTCAATGGCAGGTAGCCGATCA 3900
Db
3841 GTACGTGCTCGTCGATCGATGTTTCGCTGGTGGTCAATGGCAGGTAGCCGATCA 3900
QY
3901 AGCGTATGACGCGCGCATTCGATCAGCATGATGATGATCTTCTCGGAGGAGCAAGG 3960
Db
3901 AGCGTATGACGCGCGCATTCGATCAGCATGATGATGATCTTCTCGGAGGAGCAAGG 3960
QY
3961 TGAGATGACGAGATCCTGCGCCCGGCACTTGGCCCAATAGCAGCCAGTCCCTTCCGCT 4020
Db
3961 TGAGATGACGAGATCCTGCGCCCGGCACTTGGCCCAATAGCAGCCAGTCCCTTCCGCT 4020
QY
4021 TCAGTGACAGTTCAGACACAGCTCGCAAGAACCGGTCGTCGGCCAGCCAGATAGC 4080
Db
4021 TCAGTGACAGTTCAGACACAGCTCGCAAGAACCGGTCGTCGGCCAGCCAGATAGC 4080
QY
4081 CGCGTGTGCTGCTCTTTCAGTTCATTCAGGGCACCGGACAGTCTTGACAAAAGA 4140
Db
4081 CGCGTGTGCTGCTCTTTCAGTTCATTCAGGGCACCGGACAGTCTTGACAAAAGA 4140
QY
4141 ACCGGGCGCCCTGCGCTGACAGCGGAACACGGCGGATCAGACCGGATTCGTGT 4200
Db
4141 ACCGGGCGCCCTGCGCTGACAGCGGAACACGGCGGATCAGACCGGATTCGTGT 4200
QY
4201 TGTGCCAGTATAGCCGATAGCTCTCCACCGAGCGCGGAGAACTTCGTCGCAAT 4260
Db
4201 TGTGCCAGTATAGCCGATAGCTCTCCACCGAGCGCGGAGAACTTCGTCGTCGCAAT 4260
QY
4261 CCATCTTGTTCATCATGGAACGATCCTCATCTGCTCTTGTATCAGAGCTTCATCCC 4320
Db
4261 CCATCTTGTTCATCATGGAACGATCCTCATCTGCTCTTGTATCAGAGCTTCATCCC 4320
QY
4321 CTGCGCCATCAG 4332
Db
4321 CTGCGCCATCAG 4332

RESULT 2

ADT55136
ID ADT55136 standard; DNA; 4293 BP.
XX
AC ADT55136;
XX
DT 30-DEC-2004 (first entry)
XX
DE Nucleotide sequence of expression vector pMB1-HA-MnSOD.

XX Ophthalmological; radiation; free radical; superoxide anion;
KW heavy metal cation; metallothionein; superoxide dismutase; SOD; catalase;
KW glutathione peroxidase 4; GPx-4; gamma glutamyl transpeptidase;
KW xerostomia; xerophthalmia; autoimmune disorder; Sjogren's syndrome;
KW graft-versus-host disease; systemic lupus erythematosus;
KW rheumatoid arthritis; HIV-1 infection; ageing; autoimmune dysfunction;
KW psychogenic disorder; trauma; hepatitis C; cancer; mastication; ss.

OS Homo sapiens.
OS Simian virus 40.
OS Synthetic.

XX Key Location/Qualifiers
FT 2..781
CDS /*tag= a

FT intron /note= "human Manganese superoxide dismutase cDNA"
FT 332..497
FT /*tag= b
FT /note= "human beta-globin intron"
FT 347..503
FT /*tag= c
FT /note= "SV40 late gene polyadenylation signal"
FT 471..1162
FT /*tag= d
FT /note= "CMV promoter"
FT 1158..1825
FT /*tag= e
FT /note= "ColE1 ori from pBluescript SK+"
FT 1226..2020
FT /*tag= f
FT /gene= "kanamycin resistance gene"
PN W02004087873-A2.
XX
PD 14-OCT-2004.
XX
PF 26-MAR-2004; 2004WO-US009194.
XX
PR 26-MAR-2003; 2003US-0458793P.
PR 25-MAR-2004; 2004US-07778889.
XX
PA (GENT-) GENTERIC INC.
XX
PI Bennett MJ, Chen Y;
PI
DR WPI; 2004-737685/72.
XX
XX Attenuating increases in concentrations of radiation-induced free
radicals in a mammalian cell, comprises contacting the cell with one or
more nucleic acids encoding proteins that neutralizes or eliminates a
portion of free radicals.
PS Claim 34; SEQ ID NO 2; 58pp; English.
CC The specification describes a method for attenuating increases in
concentrations of radiation-induced free radicals, superoxide anions or
heavy metal cations in a mammalian cell. The method comprises contacting
the cell with one or more nucleic acids encoding one or more proteins
that are expressed in the cell and that neutralizes or eliminates a
portion of the free radicals, superoxide anions or heavy metal cations in
the cell. The proteins are selected from metallothionein, superoxide
dismutase, catalase, glutathione peroxidase (GPx)-4, or gamma glutamyl
transpeptidase. The method is useful for attenuating increases in
concentrations of radiation-induced free radicals, superoxide anions or
heavy metal cations in a mammalian cell, and ameliorating symptoms of
xerostomia or xerophthalmia associated with conditions such as autoimmune
disorders, Sjogren's syndrome, graft-versus-host disease, systemic lupus
erythematosus, rheumatoid arthritis, HIV-1 infection, ageing, autoimmune
dysfunction, conditions affecting the CNS, psychogenic disorder, trauma,
hepatitis C, cancer and decrease in mastication. The present sequence
represents an expression vector used in the method of the invention to
express the relevant proteins.
XX
SQ Sequence 4293 BP; 1089 A; 1090 C; 1112 G; 1001 T; 0 U; 1 Other;
Query Match 96.3%; Score 4170.6; DB 13; Length 4293;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 454; Conservative 0; Mismatches 39; Indels 39; Gaps 2;
QY 1 CGGTGCGGCGCTCTTCGCTATTACGCCAGCTCGGGAAGGGGGATGCTGCGAAGCGAT 60
Db
1 CGGTGCGGCGCTCTTCGCTATTACGCCAGCTCGGGAAGGGGGATGCTGCGAAGCGAT 60
QY 61 TAAGTTGGGTACGCCAGGGTTTTCCAGTCACAGCTTGTAAACACGCGGCAGTGAAT 120
Db
61 TAAGTTGGGTACGCCAGGGTTTTCCAGTCACAGCTTGTAAACACGCGGCAGTGAAT 120
QY 121 TGTAAATACGACTCACTATAGGGGGAATTGGGTACTGGCCACAGAGCTTGGCCCATTTGCAT 180

Db	121	TGTAATACGACTCACTATAGGCGGAATTTGGGTACTGGCCACAGAGCTTTGGCCCATTTGCAT	180
Qy	181	ACGTTGTATCCATATCAATATATGTACATTTATATTTGGCTCATGTCCAACATTTACCGCA	240
Db	181	ACGTTGTATCCATATCAATATATGTACATTTATATTTGGCTCATGTCCAACATTTACCGCA	240
Qy	241	TGTTGACATTTGATTTATTTGACTAGTTTATTAATAGTAATCAATTTACGGGCTCATTTAGTTTCAT	300
Db	241	TGTTGACATTTGATTTATTTGACTAGTTTATTAATAGTAATCAATTTACGGGCTCATTTAGTTTCAT	300
Qy	301	AGCCATATATGGAGTTCCGGTTTACATAACTTACGGTAAATTTGGCCCGCTTGGCTGACCG	360
Db	301	AGCCATATATGGAGTTCCGGTTTACATAACTTACGGTAAATTTGGCCCGCTTGGCTGACCG	360
Qy	361	CCCAACGACCCCGCCCAATGACGTCATTAATAGTATGTTTCCCATAGTAACGCCAATA	420
Db	361	CCCAACGACCCCGCCCAATGACGTCATTAATAGTATGTTTCCCATAGTAACGCCAATA	420
Qy	421	GGGACTTTTCCATTTGACGTCATTTGGGTGGAGTATTTACGGTAAACTTGGCCACTTGGCAGTA	480
Db	421	GGGACTTTTCCATTTGACGTCATTTGGGTGGAGTATTTACGGTAAACTTGGCCACTTGGCAGTA	480
Qy	481	CATCAAGTGTATCATATGCCAAGTACGCCCCCTATTTGACGTCATAGAGGTAATTTGGCCC	540
Db	481	CATCAAGTGTATCATATGCCAAGTACGCCCCCTATTTGACGTCATAGAGGTAATTTGGCCC	540
Qy	541	GCCTGGCATATGCCCAGTACATGACCTTATGGGACTTTTCCCTACTTGGCAGTACATCTAC	600
Db	541	GCCTGGCATATGCCCAGTACATGACCTTATGGGACTTTTCCCTACTTGGCAGTACATCTAC	600
Qy	601	GTATTTAGTCATCGCTATTTACCATGGTGTATGGGTTTTTGGCAGTACATCAATTTGGCGTGA	660
Db	601	GTATTTAGTCATCGCTATTTACCATGGTGTATGGGTTTTTGGCAGTACATCAATTTGGCGTGA	660
Qy	661	TAGCGGTTTGTACTACGGGATTTCCAAAGTCTCAACCCATTTGACGTCATAGAGGATTTG	720
Db	661	TAGCGGTTTGTACTACGGGATTTCCAAAGTCTCAACCCATTTGACGTCATAGAGGATTTG	720
Qy	721	TTTTGGCACAAAATCAACGGGACTTTCCAAAATGTGCTAACACTCGCCCTCATTTGACG	780
Db	721	TTTTGGCACAAAATCAACGGGACTTTCCAAAATGTGCTAACACTCGCCCTCATTTGACG	780
Qy	781	CAAAATGGCGGTAGCGGTGTACGGTGGAGGTCTATATAAGCAGAGCTCGTTTATAGTAAC	840
Db	781	CAAAATGGCGGTAGCGGTGTACGGTGGAGGTCTATATAAGCAGAGCTCGTTTATAGTAAC	840
Qy	841	CGTCAGATCGCTGGAGAGCCATCCAGCTGTTTGGACCTCCATAGAGACACCGGGAC	900
Db	841	CGTCAGATCGCTGGAGAGCCATCCAGCTGTTTGGACCTCCATAGAGACACCGGGAC	900
Qy	901	CGATCCAGCCTGACTTACGCTAGCTGTGAAGTTTGGTGGAGCCCTGGGACGTTTGGT	960
Db	901	CGATCCAGCCTGACTTACGCTAGCTGTGAAGTTTGGTGGAGCCCTGGGACGTTTGGT	960
Qy	961	ATCAAGGTTTACAGACAGGTTTAAAGGAGACCAATAGAACTGGGCACTGTGGAGACAGAGA	1020
Db	961	ATCAAGGTTTACAGACAGGTTTAAAGGAGACCAATAGAACTGGGCACTGTGGAGACAGAGA	1020
Qy	1021	AGACTCTTGGGTTTCTGATAGGCACTGACTCTCTCTGGCTATTTGGTCTATTTTCCACCC	1080
Db	1021	AGACTCTTGGGTTTCTGATAGGCACTGACTCTCTCTGGCTATTTGGTCTATTTTCCACCC	1080
Qy	1081	TTAGGCTGCTGGTCTGAGGATCTCTCGAGGTTCGACGCTATTCGATTAAGCTTTGAT	1140
Db	1081	TTAGGCTGCTGGTCTGAGGATCTCTCGAGGTTCGACGCTATTCGATTAAGCTTTGAT	1140
Qy	1141	ATCGAAATTCGGGCGGCGCAGGAGCGGCACTCGTGGCTGTGGTCTTGGCAGCGCTT	1200
Db	1141	AAATCCACCATGGCTTC-----TAGCCCTTATGACGTGCTGACTATGCGAGTTTAGG	1193
Qy	1201	CAGCAGATCGCGGCATCAGCGGTAGCACACGACTAGCAGCACTGTGAGCCCGGCGAGTG	1260

Db	1194	AGGACCTTCT-----ATGTTGAGCGCGGCACTG	1221
Qy	1261	TGCGGACACGACGAGCTGGCTCCGGTTTGGGTTATCTGGGCTCCAGGACAGAGCAC	1320
Db	1222	TGCGGACACGACGAGCTGGCTCCGGTTTGGGTTATCTGGGCTCCAGGACAGAGCAC	1281
Qy	1321	AGCCTCCCGACCTTGCCTTACGACTACGGGCGCTTGAACCTCACATCAACCGCGCAGATC	1380
Db	1282	AGCCTCCCGACCTTGCCTTACGACTACGGGCGCTTGAACCTCACATCAACCGCGCAGATC	1341
Qy	1381	ATGAGCTGACACACGACGACGCGGCTTACGTAACCACTGTAACGCTGACCGAG	1440
Db	1342	ATGAGCTGACACACGACGACGCGGCTTACGTAACCACTGTAACGCTGACCGAG	1401
Qy	1441	GAGAAGTACAGAGGAGGCTTGGCCCAAGGAGATGTTACAGCCAGATAGCTTCTCAGCCT	1500
Db	1402	GAGAAGTACAGAGGAGGCTTGGCCCAAGGAGATGTTACAGCCAGATAGCTTCTCAGCCT	1461
Qy	1501	GCATGAAGTTCAATGGTGGTGCATATCAATCATAGCATTTTCTGGACAAACCTCAGC	1560
Db	1462	GCATGAAGTTCAATGGTGGTGCATATCAATCATAGCATTTTCTGGACAAACCTCAGC	1521
Qy	1561	CCTAACCGTGGTGGAGAACCCAAAGGGAGTTGCTGGAAAGCCATCAAACTGTTGGT	1620
Db	1522	CCTAACCGTGGTGGAGAACCCAAAGGGAGTTGCTGGAAAGCCATCAAACTGTTGGT	1581
Qy	1621	TCCTTTGACAAAGTTTAAAGGAGAGCTGACGCTGCATCTGTTGGTGTCCAGGCTCAGGT	1680
Db	1582	TCCTTTGACAAAGTTTAAAGGAGAGCTGACGCTGCATCTGTTGGTGTCCAGGCTCAGGT	1641
Qy	1681	TGGGTTTGGCTTGGTTTCAATAAGGAAACGGGGAACCTTACAAATTTGCTGTGTTCCAAAT	1740
Db	1642	TGGGTTTGGCTTGGTTTCAATAAGGAAACGGGGAACCTTACAAATTTGCTGTGTTCCAAAT	1701
Qy	1741	CAGATCCACTGCAGAGAACCAACGGGCTTATTTCCACTGCTGGGGATTTGATGTGGAG	1800
Db	1702	CAGATCCACTGCAGAGAACCAACGGGCTTATTTCCACTGCTGGGGATTTGATGTGGAG	1761
Qy	1801	CAGCTTACTACCTTTCAGTATAAAATGTTCAGGCTGATTTATCTAAAGCTTATTTGGAAAT	1860
Db	1762	CAGCTTACTACCTTTCAGTATAAAATGTTCAGGCTGATTTATCTAAAGCTTATTTGGAAAT	1821
Qy	1861	GTAAATCAACTGGGAGAAATGTAACTGAAAGATACATGCTTGTGAAAAAGTAAACCCAGAT	1920
Db	1822	GTAAATCAACTGGGAGAAATGTAACTGAAAGATACATGCTTGTGAAAAAGTAAACCCAGAT	1881
Qy	1921	CGTTATGCTCGAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANA	1980
Db	1882	CGTTATGCTCGAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANA	1941
Qy	1981	AAAAAACGGAAATTCCTGACGCGCGGGGATCCACTAGTTCTAGAGCGCGCCACCGCG	2040
Db	1942	AAAAAACGGAAATTCCTGACGCGCGGGGATCCACTAGTTCTAGAGCGCGCCACCGCG	2001
Qy	2041	GTGAGCTCCCAACTAGAAATGCAAGTGAANAANAANAANAANAANAANAANAANAANA	2100
Db	2002	GTGAGCTCCCAACTAGAAATGCAAGTGAANAANAANAANAANAANAANAANAANAANA	2061
Qy	2101	TATTTGCTTTATTTGTTAACTGCAATTAAGCTGCAATTAAGCTGCAATTAAGCTGCAATTA	2160
Db	2062	TATTTGCTTTATTTGTTAACTGCAATTAAGCTGCAATTAAGCTGCAATTAAGCTGCAATTA	2121
Qy	2161	TTTTTATGTTTTCAGGTTTCAGGGGAGGTTTGGGAGGTTTTTAAAGCCACAGCTCCAGCTT	2220
Db	2122	TTTTTATGTTTTCAGGTTTCAGGGGAGGTTTGGGAGGTTTTTAAAGCCACAGCTCCAGCTT	2181
Qy	2221	TTGTTCCCTTTTATGAGGTTTAAATTTTCGAGCTTGGGCTGATTAATCATAGCTGTTTTC	2280
Db	2182	TTGTTCCCTTTTATGAGGTTTAAATTTTCGAGCTTGGGCTGATTAATCATAGCTGTTTTC	2241
Qy	2281	TGTTGTAATTTGTTATCCGCTCAAAATTTCCACACATACGAGCGCGGAGCATTAAGTG	2340
Db	2242	TGTTGTAATTTGTTATCCGCTCAAAATTTCCACACATACGAGCGCGGAGCATTAAGTG	2301

QY 1321 AGCCTCCCGACCTGCTTACGACTAGCGGCCCTTGGAACTCATCAACGCGCAGATC 1380
 DB 1321 TGGG- CGCGCGGAGCCCGGGTACCGGCTGCTCTTCCGCGCAGCTTGGCGCCCGC 1379
 QY 1381 ATGAGCTGCAACACAGCAAGCAACGCGGCCCTACGTGAACAACCTGAAAGTCAACGAG 1440
 DB 1380 GCCAAGCTCGACGCGCTTCTTCGCGCTGAGGGCTTCCGACCGAGCGGAAACAGCTCC-AG 1438
 QY 1441 GAGAAGTACAGAGGCGTTCGCCCAAGGAGATGTTACAGCCAGATAGCTCTTCAGCCT 1500
 DB 1439 CCGCGCCATCCAGGTGCAACCAAGTTCGGGGACCTGAGCCAGGCTGCGAGTCCACCGGGCC 1498
 QY 1501 GCACCTGAAGTCAATGTGTGTGTCATATCAATCATAGCATTTTCTGGACAAACCTCAGC 1560
 DB 1499 CCACCTACACCGCTGGCG- - - - - TGGCGCACCGCGAGC 1533
 QY 1561 CCTAACGCTGTGGAGAACCCAAAGGGAGTGTGCTGGAAGCATCAACGCTGACTTTGGT 1620
 DB 1534 ACCGGGCGACTTCGGCAACTTCGCGTCCGCGACGGCAGCTCTGGAGGTACCGCGCG 1593
 QY 1621 TCCTTTGACAAGTTTAAGAGAGCTGACGCTGCATCTGTGTGTCCTCAAGGCTCAGGT 1680
 DB 1594 GCCT- - - - - GCGCGCTCGCTCGCGGCGCCGCACTCCATC 1628
 QY 1681 TGGGCTTGGCTTGTTCATAAAGNAAGGGGACACTTACAAATTTGCTGTGTCCAAAT 1740
 DB 1629 GTGGCGCGGCG- - - - - TGGTCTCCACGCTGGCGAGGACGACCTGGGCGCGG 1678
 QY 1741 CAGGATCCACTGCAAGGAACACAGGCTTATTCACCTGCTGGGATGTGTGTGGAG 1800
 DB 1679 CGGCAACAGGCGACGCTGGAGACG- - - - - GGNACGGCGGCGC 1717
 QY 1801 CACGCTTACTACTTCAGTATAAATAATGTCAGGCTGATTAATCAAAAGCTATTTGGAAT 1860
 DB 1718 GCGGCTGGCTGCTCGTGTGGGCGTGTGGGCGCGGCTCTGGGAGCGCAGCGCG 1777
 QY 1861 GTAATCAATCGGGAGAAATGTAATGAAAGATACATGCTTGCAAAAAAGTAAACACGAT 1920
 DB 1778 GGAGCACTCAGACGCAAGAACGCGCGCGAGAGCGAGTGAAGCGCGCTGAAAGCT 1837
 QY 1921 CQTATGCTGGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1980
 DB 1838 TGATATCG- - - - - 1845
 QY 1981 AAAAAAGGAATTCCTGCGAGCCCGGGGATCCACTAGTTCCTAGAGCGCGCCACCGCG 2040
 DB 1846 - - - - - AATTCTGCGAGCCCGGGGATCCACTAGTTCCTAGAGCGCGCCACCGCG 1895
 QY 2041 GTGAGCTCCAACTAGAAATCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGC 2100
 DB 1896 GTGAGCTCCAACTAGAAATCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGC 1955
 QY 2101 TATTGCTTTATTGTAAACCAATTAAGCTGCAATAAACAAGTTAAACAATTTGCAATCA 2160
 DB 1956 TATTGCTTTATTGTAAACCAATTAAGCTGCAATAAACAAGTTAAACAATTTGCAATCA 2015
 QY 2161 TTTTATGTTTCAAGTTTCAAGGGAGGTGTGGAGGTTTTTTTAAAGCCACAGCTCCAGCTT 2220
 DB 2016 TTTTATGTTTCAAGTTTCAAGGGAGGTGTGGAGGTTTTTTTAAAGCCACAGCTCCAGCTT 2075
 QY 2221 TTGTTCCCTTTAGTAGGTTTAAATTCGAGCTTGGCGTAAATCATGTTGATGTTTCC 2280
 DB 2076 TTGTTCCCTTTAGTAGGTTTAAATTCGAGCTTGGCGTAAATCATGTTGATGTTTCC 2135
 QY 2281 TGTGTGAATTTGTTATCCGCTCACAATCCACACATACGAGCCGGAAGCATAAGTG 2340
 DB 2136 TGTGTGAATTTGTTATCCGCTCACAATCCACACATACGAGCCGGAAGCATAAGTG 2195
 QY 2341 TAAAGCTCGGGTGCCTAATGAGTGAGCTAACTCACATTAATTTGCGTTGCGTCACTGCC 2400
 DB 2196 TAAAGCTCGGGTGCCTAATGAGTGAGCTAACTCACATTAATTTGCGTTGCGTCACTGCC 2255

QY 2401 CGCTTCCAGTCGGGAAACCTGCTGCGAGCTGCATTAATGATCGGCGCAACGCGCGG 2460
 DB 2256 CGCTTCCAGTCGGGAAACCTGCTGCGAGCTGCATTAATGATCGGCGCAACGCGCGG 2315
 QY 2461 GAGAGCGGTTTGGTATTTGGGCGCTCTTCGCTTCTCGTCACTGCTGCTGCGCTC 2520
 DB 2316 GAGAGCGGTTTGGTATTTGGGCGCTCTTCGCTTCTCGTCACTGCTGCTGCGCTC 2375
 QY 2521 GGTGTTTGGCTGCGGAGCGGTATCAGTCACTCAAAAGCGGTATACGGTTATCCAC 2580
 DB 2376 GGTGTTTGGCTGCGGAGCGGTATCAGTCACTCAAAAGCGGTATACGGTTATCCAC 2435
 QY 2581 AGAATCAGGGGATTAACCCAGGAAGACATGTGAGCAAAAGGCCAGCAAAAGGCCAGAA 2640
 DB 2436 AGAATCAGGGGATTAACCCAGGAAGACATGTGAGCAAAAGGCCAGCAAAAGGCCAGAA 2495
 QY 2641 CCGTAAAAAGCGCGCTTGTGCGGCTTTTCCATAGGCTCCGCCCTCTGACGAGCATCA 2700
 DB 2496 CCGTAAAAAGCGCGCTTGTGCGGCTTTTCCATAGGCTCCGCCCTCTGACGAGCATCA 2555
 QY 2701 CAAAAATCGACGCTCAAGTCAAGGTGCGGAAACCCGACAGGACTATAAAGATACAGGC 2760
 DB 2556 CAAAAATCGACGCTCAAGTCAAGGTGCGGAAACCCGACAGGACTATAAAGATACAGGC 2615
 QY 2761 GTTTCCCGCTGGAAGCTCCCTCGTCCGCTCTCCTGTTCCGACCTCGCGCTTACCGGATA 2820
 DB 2616 GTTTCCCGCTGGAAGCTCCCTCGTCCGCTCTCCTGTTCCGACCTTCCCGCTTACCGGATA 2675
 QY 2821 CCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCAATGCTCACGCTGTAGTA 2880
 DB 2676 CCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCAATGCTCACGCTGTAGTA 2735
 QY 2881 TCTCAGTTCGCTGAGTGTGCTCCAACTGCGGCTGTGTGACGAAACCCCGCTTCA 2940
 DB 2736 TCTCAGTTCGCTGAGTGTGCTCCAACTGCGGCTGTGTGACGAAACCCCGCTTCA 2795
 QY 2941 GCCGACGCTCGCGCTTATCCGCTTAACTATCGTCTGAGTCCAAACCGGTAAAGACAGA 3000
 DB 2796 GCCGACGCTCGCGCTTATCCGCTTAACTATCGTCTGAGTCCAAACCGGTAAAGACAGA 2855
 QY 3001 CTTATCGCACTGCGCAGCAGCACTGGTAAACAGGATTAAGCAGAGCGAGTATGTAGCGG 3060
 DB 2856 CTTATCGCACTGCGCAGCAGCACTGGTAAACAGGATTAAGCAGAGCGAGTATGTAGCGG 2915
 QY 3061 TGCTACAGAGTCTTGAAGTGTGCGCTTAACTACGCTTACACTAGAGCAGAGTATTTGG 3120
 DB 2916 TGCTACAGAGTCTTGAAGTGTGCGCTTAACTACGCTTACACTAGAGCAGAGTATTTGG 2975
 QY 3121 TATCTGCGCTCTGCTGAAGCCAGTTCCTTCGGAATAAGAGTGTGCTTGTATCCCG 3180
 DB 2976 TATCTGCGCTCTGCTGAAGCCAGTTCCTTCGGAATAAGAGTGTGCTTGTATCCCG 3035
 QY 3181 CAAAAACCAACCGCTGCTGAGCGGTGTTTTTTTTCGCAAGCAGCAGATTAACGCGAG 3240
 DB 3036 CAAAAACCAACCGCTGCTGAGCGGTGTTTTTTTTCGCAAGCAGCAGATTAACGCGAG 3095
 QY 3241 AAAAAAGGATCTCAAGAGATCTCTTTGATCTTTTCTACGCGGTCTGACGCTCAGTGGAA 3300
 DB 3096 AAAAAAGGATCTCAAGAGATCTCTTTGATCTTTTCTACGCGGTCTGACGCTCAGTGGAA 3155
 QY 3301 CGAAAACTCAGCTTAAGGATTTTGTCTATGAGCGGATACATATTTGAATGTATTAGAA 3360
 DB 3156 CGAAAACTCAGCTTAAGGATTTTGTCTATGAGCGGATACATATTTGAATGTATTAGAA 3215
 QY 3361 AAATAAACAAATAGGGTTCCCGCACATTTCCCGGAAAGTGCACCTGTATGCGGTGT 3420
 DB 3216 AAATAAACAAATAGGGTTCCCGCACATTTCCCGGAAAGTGCACCTGTATGCGGTGT 3275
 QY 3421 GAAATACCGCAGAGTGTGAGGAAATAACCGCATCAGGAAATTTGAAGGTTTAATA 3480
 DB 3276 GAAATACCGCAGAGTGTGAGGAAATAACCGCATCAGGAAATTTGAAGGTTTAATA 3335
 QY 3481 ATTCAGAAAGACTCGTCAAGAGGCGGATAGAAAGGCGATGCGCTGCGAATCGGAGCGCG 3540

Db 3336 ATTCAGAAAGTCTGTCAGAGCGGATAGAGCGGATGCGTCGGAATCGGAGCGCG 3395
QY 3541 ATACCGGTAAAGCAGAGGAGCGGTACGCCATTCGGCGGCAAGCTCTTCAGCAATATCA 3600
Db 3396 ATACCGGTAAAGCAGAGGAGCGGTACGCCATTCGGCGGCAAGCTCTTCAGCAATATCA 3455
QY 3601 CGGTAGCCAAACGCTATGCTCTGATAGCGGTCCGCCACACCCAGCGGCCACAGTCGATG 3660
Db 3456 CGGTAGCCAAACGCTATGCTCTGATAGCGGTCCGCCACACCCAGCGGCCACAGTCGATG 3515
QY 3661 AATCCAGAAAGCGGCCATTTCCACATGATATTCGGCAAGCAGGCAATCGCCATGGGTC 3720
Db 3516 AATCCAGAAAGCGGCCATTTCCACATGATATTCGGCAAGCAGGCAATCGCCATGGGTC 3575
QY 3721 ACAGCAGATCTCTCGCGTGGGATGCTCGCTTGGAGCGCTGGCGAAGCAGTCTGGCTGGC 3780
Db 3576 ACAGCAGATCTCTCGCGTGGGATGCTCGCTTGGAGCGCTGGCGAAGCAGTCTGGCTGGC 3635
QY 3781 GCGAGCCCTGATGCTCTTCTGTCAGATCATCTGATCGACAGACCGGCTTCCATCCGA 3840
Db 3636 GCGAGCCCTGATGCTCTTCTGTCAGATCATCTGATCGACAGACCGGCTTCCATCCGA 3695
QY 3841 GTAGTCTCTGCTCGATGCGATGTTTCGTTGGTGGTTCGAATGGCGAGGTAGCCGATCA 3900
Db 3696 GTAGTCTCTGCTCGATGCGATGTTTCGTTGGTGGTTCGAATGGCGAGGTAGCCGATCA 3755
QY 3901 AGGTATGACAGCGCCGATTCGATCAGCATGATGATGATGATGATGATGATGATGATG 3960
Db 3756 AGGTATGACAGCGCCGATTCGATCAGCATGATGATGATGATGATGATGATGATGATG 3815
QY 3961 TGAGATGACAGGAGATCTGCGCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCT 4020
Db 3816 TGAGATGACAGGAGATCTGCGCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCT 3875
QY 4021 TCAGTGAACAGTTCGACGACGATGCGCAAGGAAAGCGCCGTCGTGGCCAGCCAGTATG 4080
Db 3876 TCAGTGAACAGTTCGACGACGATGCGCAAGGAAAGCGCCGTCGTGGCCAGCCAGTATG 3935
QY 4081 CGCGTCTCTCTCTTCAGTTCATTCAGGCGACCGGACAGGTCGGTCTTGCACAAAGA 4140
Db 3936 CGCGTCTCTCTCTTCAGTTCATTCAGGCGACCGGACAGGTCGGTCTTGCACAAAGA 3995
QY 4141 ACCGGCGCCCTCGCTGCTGACGCGGAAACACGCGGCATCAGACGCGGATGTTCTGT 4200
Db 3996 ACCGGCGCCCTCGCTGCTGACGCGGAAACACGCGGCATCAGACGCGGATGTTCTGT 4055
QY 4201 TGTGCCAGTCATGCGGAATAGCTCTCCACCAAGCGCGGAGAACCTGCGTGAAT 4260
Db 4056 TGTGCCAGTCATGCGGAATAGCTCTCCACCAAGCGCGGAGAACCTGCGTGAAT 4115
QY 4261 CCATCTTGTTCATGCGAAACGATCCTCATCTCTCTTGTATCAGAGTTGATCCC 4320
Db 4116 CCATCTTGTTCATGCGAAACGATCCTCATCTCTCTTGTATCAGAGTTGATCCC 4175
QY 4321 CTGCGCCATCAG 4332
Db 4176 CTGCGCCATCAG 4187

RESULT 4

ADT55139

ID ADT55139 standard; DNA; 4058 BP.

AC ADT55139;

XX ADT55139;

XX ADT55139;

DT 30-DEC-2004 (first entry)

XX Nucleotide sequene of expression vector pMB1-hlFNalpha.

XX Ophthalmological; radiation; free radical; superoxide anion;

KW heavy metal cation; metallothionein; superoxide dismutase; SOD; catalase;

KW glutathione peroxidase 4; GPX-4; gamma glutamyl transpeptidase;

KW xerostomia; xerophthalmia; autoimmune disorder; Sjogren's syndrome;
KW graft-versus-host disease; systemic lupus erythematosus;
KW rheumatoid arthritis; HIV-1 infection; ageing; autonomic dysfunction;
XX psychogenic disorder; trauma; hepatitis C; cancer; mastication; ss.
OS Homo sapiens.
OS Simian virus 40.
XX Synthetic.
PH Key Location/Qualifiers
FT intron 332..497.
FT /*tag= a
FT FT /*note= "human beta-globin intron"
FT polyA_signal 347..503
FT /*tag= b
FT /*note= "SV40 late gene polyadenylation signal"
FT promoter 471..1162
FT /*tag= c
FT /*note= "CMV promoter"
FT CDS 551..1077
FT /*tag= d
FT /*note= "human interferon (IFN) alpha cDNA"
FT rep_origin 1158..1825
FT /*tag= e
FT /*note= "ColE1 ori from pBluescript SK+"
FT CDS 1226..2020
FT /*tag= f
FT /*gene= "kanamycin resistance gene"
XX WO2004087873-A2.
XX 14-OCT-2004.
XX 26-MAR-2004; 2004WO-US009194.
XX 26-MAR-2004; 2003US-0458793P.
XX 25-MAR-2004; 2004US-0777889.
XX (GENT-) GENTERIC INC.
XX Bennett MJ, Chen Y;
XX WPI; 2004-737685/72.
XX Attenuating increases in concentrations of radiation-induced free
PT radicals in a mammalian cell, comprises contacting the cell with one or
PT more nucleic acids encoding proteins that neutralizes or eliminates a
XX portion of free radicals.
XX Claim 34; SEQ ID NO 5; 58pp; English.
XX The specification describes a method for attenuating increases in
CC concentrations of radiation-induced free radicals, superoxide anions or
CC heavy metal cations in a mammalian cell. The method comprises contacting
CC the cell with one or more nucleic acids encoding one or more proteins
CC that are expressed in the cell and that neutralizes or eliminates a
CC portion of the free radicals, superoxide anions or heavy metal cations in
CC the cell. The proteins are selected from metallothionein, superoxide
CC dismutase, catalase, glutathione peroxidase (GPX)-4, or gamma glutamyl
CC transpeptidase. The method is useful for attenuating increases in
CC concentrations of radiation-induced free radicals, superoxide anions or
CC heavy metal cations in a mammalian cell, and ameliorating symptoms of
CC xerostomia or xerophthalmia associated with conditions such as autoimmune
CC disorders, Sjogren's syndrome, graft-versus-host disease, systemic lupus
CC erythematosus, rheumatoid arthritis, HIV-1 infection, ageing, autonomic
CC dysfunction, conditions affecting the CNS, psychogenic disorder, trauma,
CC hepatitis C, cancer and decrease in mastication. The present sequence
CC represents an expression vector used in the method of the invention to
XX express the relevant proteins.
SQ Sequence 4058 BP; 999 A; 1038 C; 1051 G; 970 T; 0 U; 0 Other;
Query Match 72.7%; Score 3147.8; DB 13; Length 4058;

Best Local Similarity 85.6%; Pred. No. 0;
Matches 3710; Conservative 0; Mismatches 348; Indels 274; Gaps 8;

Qy	1	CGGTGGGGCTCTTTCGCTATATACGCCAGCTGCGGAAGGGGGATGCTGCTCAAGCGCAT	60
Db	1	CGGTGGGGGGCTCTTCGCTATATACGCCAGCTGCGGAAGGGGGATGCTGCTCAAGCGCAT	60
Qy	61	TAAGTTGGGTAAACGCCACAGGGTTTTCCAGTCAACGAGTGTGTAAACGACGGCCAGTGAAT	120
Db	61	TAAGTTGGGTAAACGCCACAGGGTTTTCCAGTCAACGAGTGTGTAAACGACGGCCAGTGAAT	120
Qy	121	TGTAATACGACTCACTATAGGGCGAATTTGGGTACTGGCCACAGAGCTTTGGCCCATTTGCAT	180
Db	121	TGTAATACGACTCACTATAGGGCGAATTTGGGTACTGGCCACAGAGCTTTGGCCCATTTGCAT	180
Qy	181	ACGTTGTATCCATATCATATAATGTACATTTATTTGGCTCATGTCCAAATTTACCGCCA	240
Db	181	ACGTTGTATCCATATCATATAATGTACATTTATTTGGCTCATGTCCAAATTTACCGCCA	240
Qy	241	TGTTGACATTTGATTTGACTAGTTATTAATAGTAATCAATTAACGGGGTCATTTAGTTTCAT	300
Db	241	TGTTGACATTTGATTTGACTAGTTATTAATAGTAATCAATTAACGGGGTCATTTAGTTTCAT	300
Qy	301	AGCCATATATGGAGTTCCGCGTTTACATACTTTACGGTAAATGCCCGCTGGCTGACCG	360
Db	301	AGCCATATATGGAGTTCCGCGTTTACATACTTTACGGTAAATGCCCGCTGGCTGACCG	360
Qy	361	CCCAACGACCCCGCCCATTTGACGTCAATAATGACGTATGTTCCCATAGTAAACGCCAAATA	420
Db	361	CCCAACGACCCCGCCCATTTGACGTCAATAATGACGTATGTTCCCATAGTAAACGCCAAATA	420
Qy	421	GGGACTTTTCCATTTGACGTCAATGGTGGAGTATTTACGGTAAATCTGCCACTTTGGCAGTA	480
Db	421	GGGACTTTTCCATTTGACGTCAATGGTGGAGTATTTACGGTAAATCTGCCACTTTGGCAGTA	480
Qy	481	CATCAAGTGTATCATATATGCCAAGTACGCCCCCTTATTCAGTCAATGACGGTAAATGGCCCC	540
Db	481	CATCAAGTGTATCATATATGCCAAGTACGCCCCCTTATTCAGTCAATGACGGTAAATGGCCCC	540
Qy	541	GCCTGGCATTTATGCCAGTACATGACCTTTATGGAGCTTTCTACTTTGGCAGTACATCTAC	600
Db	541	GCCTGGCATTTATGCCAGTACATGACCTTTATGGAGCTTTCTACTTTGGCAGTACATCTAC	600
Qy	601	GTATTAGTCAATCGCTATTACCATGGTGAATGGGTTTTTGGCAGTACATCAATGGCGGTGGA	660
Db	601	GTATTAGTCAATCGCTATTACCATGGTGAATGGGTTTTTGGCAGTACATCAATGGCGGTGGA	660
Qy	661	TAGCGGTTTGACTCAGCGGGATTTCAAAGTCTCAACCCCATTTGACGTCAATGGGAGTTTG	720
Db	661	TAGCGGTTTGACTCAGCGGGATTTCAAAGTCTCAACCCCATTTGACGTCAATGGGAGTTTG	720
Qy	721	TTTTTGGCACCAAAATCAACGGGACTTTTCAAAATGTGTAACTACCTCCGCCCATTTGACG	780
Db	721	TTTTTGGCACCAAAATCAACGGGACTTTTCAAAATGTGTAACTACCTCCGCCCATTTGACG	780
Qy	781	CAAAATGGCGGTAGCGGTGTAACGGTGGAGGTCTATATTAAGCAGAGCTCGTTTAGTGAAC	840
Db	781	CAAAATGGCGGTAGCGGTGTAACGGTGGAGGTCTATATTAAGCAGAGCTCGTTTAGTGAAC	840
Qy	841	CGTCAGATCGCTCGGACGCCATCCAGCTGTTTTGACCTTCCATAGAAGACACCGGGAC	900
Db	841	CGTCAGATCGCTCGGACGCCATCCAGCTGTTTTGACCTTCCATAGAAGACACCGGGAC	900
Qy	901	CGATCCAGCCTGACTCTAGCCCTAGCTCTGAAGTTGGTGGTGAAGCCCTGGCAGGTTGGT	960
Db	901	CGATCCAGCCTGACTCTAGCCCTAGCTCTGAAGTTGGTGGTGAAGCCCTGGCAGGTTGGT	960
Qy	961	ATCAAGGTTTACAAGCAGGTTTTAGGAGACCAATAGAACTGGCGCATGTGGAGACAGAGA	1020
Db	961	ATCAAGGTTTACAAGCAGGTTTTAGGAGACCAATAGAACTGGCGCATGTGGAGACAGAGA	1020
Qy	1021	AGACTCTTTGGGTTTTCTGATAGGCACATGACTCTCTCTGCTTATTTGGTCTATTTTCCCAACC	1080

1021	AGACTCTTGGGTTCTGATAGGCACTGACTCTCTCTGCGCTATTGGTCTATTTTCCACCC	1081
1081	TTAGGCTGCTGCTGAGCCTTAGGAGATCTCTCGAGGTCGACGGTATCGATAAGCTTGAT	1140
1081	TTAGGCTGCTGCTGAGCCTTAGGAGATCTCTCGAGGTCGACGGTATCGATAAGCTTGAT	1140
1141	ATCGAATTCGGGCGCGCAGGACGGGCACTCGTGGCTGTGTGGCTTCGGCAGCGGCTT	1200
1141	ATCACAGAGGAGACCATGGCTTGACCTTTGCTTTACTGGTGGCCCTCTGCTGC-----	1195
1201	CAGCAGATCGGCGGCATCAGCGGTAGCACAGCACTAGCAGCATGTTTGACCGCGGCAGTG	1260
1196	-----TCAGCTCGAAAGTCAAGCTGCTCTGTGGCTGTGATCTG	1233
1261	TGGGCACCAAGCAGGCTGGCTCCGGTTTTGGGGTATCTGGGCTTCAGGCAAGAGCAC	1320
1234	CCTCAACCCACAG-----CCTGGGTAGCAGGAGGACCTTGTG	1269
1321	AGCCTCCCGACCTGCCCTACGACTACGGCGCCTGGAACTCATCAACGGCGCAGATC	1380
1270	ATGCTCTGSCACAG-----ATGAGGAGATC	1296
1381	ATCGAGCTGCACACAGCAGCAGCACCGCGGCTACGTGAACAACTGAACGTCACCGAG	1440
1297	TCTCTTTTCTCTGCTTGAAGGACAGACATGACTTTGGATTTCCCGCAGAGGAGTTTGGC	1356
1441	GAGAAGTACCAGGAGCGGTTGGCCAAAGGGAGATGTTACAGCCAGATAGCTTTCAGCCT	1500
1357	AACGAGTTCCAAAGGCTGAACCA-----	1381
1501	GCAGTGAAGTTCAATGGTGGTGTGTCATCAATCATAGATGATTTCTTGGACAAACCTCAGC	1560
1382	-----TCCCTGTCTCTCATGAGATGATCCAGCAGATCTTCCAAT	1419
1561	CCTAAACGGTGTGGAGAACCCAAAGGGAGTGTCTGGAAGCCATCAAACTGACTTTGGT	1620
1420	CTCTTACGACAAAGGACTCATCTGCTGCTTGGGATGAGACCTCTCTAGACAAATCTAC	1479
1621	TCCTTTTGACAAGTTTAAAGGAGAAGCTGACGGCTGCAATCTGTTGGTGTCCAAGGCTCAGGT	1680
1480	ACTGAATCTTACAGCAGCTGAATGACTCGAAAGCCCTGTGT-----GATACAGGGGGT	1532
1681	TGGGTGGCTTGGTTTCAATAGGACAGCGGGACACTTACAAATGCTGCTTGTCCAAAT	1740
1533	GGGGTGCACAGAGACTCCCTGATGAAGGAGGACTC-----	1568
1741	CAGGATCCACTGCAAGGAACAACAGGCGCTTATTCCAATGCTGGGGATGATGTTGGGAG	1800
1569	-----CATTTGGCTGTGAGGAATACTTCCAAAGA	1599
1801	CAGCTTACTACTTTCAGTATAAATGTTCAGGCTGATTTATCTAAGGCTATTTTGGAAT	1860
1600	ATCACTCTCTATCTGAAGAAGAAATACAGCCCTTGTGCTGGGAGGTTGTCCAGAGCA	1659
1861	GTAATCAACTGGGAGAAATGTACTGAAGATACATGGCTTGCAAAAGATAAACACCAT	1920
160	GAATCA-----TGAGAT	1672
1921	CGTTATGCTGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1980
1673	CTTTTCTTTGTCACAAACTTGCAAGAAAGTTTAAAGAGTAAGGAATAGAAATCGTTTC	1732
1981	AAAAACGGAATTCCTGCAGCCCGGGGATCCCACTAGTTCTAGAGCGGCGCCACCGCG	2040
1733	AA-----CATGGAATGAGCTAGAGCGGCGCCACCGCG	1766
2041	GTGGAGCTCCAACTAGAATGCAGTGAATAAATAATGCTTTATTTGTGAATTTGTGATGC	2100
1767	GTGGAGCTCCAACTAGAATGCAGTGAATAAATAATGCTTTATTTGTGAATTTGTGATGC	1826
2101	TATTGCTTTATTGTGAACCATTAAGCTGCATAAACAAGTTAAACACAAATTCATTC	2160
1827	TATTGCTTTATTGTGAACCATTAAGCTGCATAAACAAGTTAAACACAAATTCATTC	1886

QY	2161	TTTTATGTTTCAGGTTTCAGGGGAGGTGTGGAGGTTTTTTTAAAGCCACAGCTCCAGCTT	2220
Db	1887	TTTTATGTTTCAGGTTTCAGGGGAGGTGTGGAGGTTTTTTTAAAGCCACAGCTCCAGCTT	1946
QY	2221	TTGTTCCCTTTAGTGAGGGTTAAATTCAGAGCTTCGGCGTAATCAATGTCATAGCTGTTTCC	2280
Db	1947	TTGTTCCCTTTAGTGAGGGTTAAATTCAGAGCTTCGGCGTAATCAATGTCATAGCTGTTTCC	2006
QY	2281	TGTGTGAATTTGTTATCGGCTCAAAATTCACACAAATACGAGCCGGAAGCATAAAGTG	2340
Db	2007	TGTGTGAATTTGTTATCGGCTCAAAATTCACACAAATACGAGCCGGAAGCATAAAGTG	2066
QY	2341	TAAAGCCTCGGGTGCCCTAAATGAGTGAGCTAACTCACATTAATTCGCTTGCGCTCACTGCC	2400
Db	2067	TAAAGCCTCGGGTGCCCTAAATGAGTGAGCTAACTCACATTAATTCGCTTGCGCTCACTGCC	2126
QY	2401	CGCTTTCAGTTCGGGAACCTGTGCTGCCAGCTGCATTAATGAATTCGGCAACGCGCGG	2460
Db	2127	CGCTTTCAGTTCGGGAACCTGTGCTGCCAGCTGCATTAATGAATTCGGCAACGCGCGG	2186
QY	2461	GAGAGCGGTTTGCGTATTCGGCGCTCTTCGGCTTCCTCGCTCACTCACTCGCTGCGCTC	2520
Db	2187	GAGAGCGGTTTGCGTATTCGGCGCTCTTCGGCTTCCTCGCTCACTCACTCGCTGCGCTC	2246
QY	2521	GGTCGTTTCGGCTGCGCGAGCGGTATCAGCTCACTCAAAGCGGTAATAATCGTTATCCAC	2580
Db	2247	GGTCGTTTCGGCTGCGCGAGCGGTATCAGCTCACTCAAAGCGGTAATAATCGTTATCCAC	2306
QY	2581	AGAAATCAGGGATNAACGAGAAAGAAACATGTGAGCAAAAGGCGCAAAAGGCCAGGAA	2640
Db	2307	AGAAATCAGGGATNAACGAGAAAGAAACATGTGAGCAAAAGGCGCAAAAGGCCAGGAA	2366
QY	2641	CCGTAAAGGCGCGTTGCGTTCGGGTTTTTCCATAGGCTCGGCCCCCTCAACAGCATCA	2700
Db	2367	CCGTAAAGGCGCGTTGCGTTCGGGTTTTTCCATAGGCTCGGCCCCCTCAACAGCATCA	2426
QY	2701	CAAAATTCAGCGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAAGATACCAAGC	2760
Db	2427	CAAAATTCAGCGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAAGATACCAAGC	2486
QY	2761	GTTCCTCCCTTGGAAGCTCCCTGTCGCTCTCTGTTCCGACCTGCGCTTACCGGATA	2820
Db	2487	GTTCCTCCCTTGGAAGCTCCCTGTCGCTCTCTGTTCCGACCTGCGCTTACCGGATA	2546
QY	2821	CTGTGCGCTTTCCTCCCTTCGGAAGCGTGGCGCTTTCTCAATGCTCAGCTGTAGGTA	2880
Db	2547	CTGTGCGCTTTCCTCCCTTCGGAAGCGTGGCGCTTTCTCAATGCTCAGCTGTAGGTA	2606
QY	2881	TCTCAGTTTCGGTGTAGGTTCGCTCAAGCTGGGCTGTGTGCAAGAACCCCGCTTCA	2940
Db	2607	TCTCAGTTTCGGTGTAGGTTCGCTCAAGCTGGGCTGTGTGCAAGAACCCCGCTTCA	2666
QY	2941	GCCGACCGCTGCGCTTATCCGGTAACATGCTTTGAGTCCAAACCCGGTAAGACAGA	3000
Db	2667	GCCGACCGCTGCGCTTATCCGGTAACATGCTTTGAGTCCAAACCCGGTAAGACAGA	2726
QY	3001	CTTATCGCCACTGCGACGCACTGTAACAGATTTAGCAGCGGAGGTATGTCAGCGG	3060
Db	2727	CTTATCGCCACTGCGACGCACTGTAACAGATTTAGCAGCGGAGGTATGTCAGCGG	2786
QY	3061	TGCTACAGAGTTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGGACAGTATTTGG	3120
Db	2787	TGCTACAGAGTTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGGACAGTATTTGG	2846
QY	3121	TATCTGCGCTCTGCTGAGCCAGTTACTTCGGAAAAAGATGGTAGCTCTTGTATCCGG	3180
Db	2847	TATCTGCGCTCTGCTGAGCCAGTTACTTCGGAAAAAGATGGTAGCTCTTGTATCCGG	2906
QY	3181	CAAAACAAACCAACCGCTGAGCGGTGGTTTTTTTGTGTAAGCAGCAGATTAACGCGCAG	3240
Db	2907	CAAAACAAACCAACCGCTGAGCGGTGGTTTTTTTGTGTAAGCAGCAGATTAACGCGCAG	2966

QY	3241	AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTTCTGACGCTCAGTGGAA	3300
Db	2967	AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTTCTGACGCTCAGTGGAA	3026
QY	3301	CGAAAACTCAGTTAAAGGATTTTGGTTCATGAGCGGATACATATTTGAATGTATTAGAA	3360
Db	3027	CGAAAACTCAGTTAAAGGATTTTGGTTCATGAGCGGATACATATTTGAATGTATTAGAA	3086
QY	3361	AAATAACAAATAGGGTTTCGCGCACATTTCCCGAAAAAGTCCACCTGTATGCGGTGT	3420
Db	3087	AAATAACAAATAGGGTTTCGCGCACATTTCCCGAAAAAGTCCACCTGTATGCGGTGT	3146
QY	3421	GAATAACCGCACAGATGCGTAAGAGAAATAACGATCAGGAAATTTGAAGCGTTAATA	3480
Db	3147	GAATAACCGCACAGATGCGTAAGAGAAATAACGATCAGGAAATTTGAAGCGTTAATA	3206
QY	3481	ATTTCAGAGAAATCTGCTCAAGAAGCGGATAGAAAGCGATGCGTGCGAATCGGGAGCGCG	3540
Db	3207	ATTTCAGAGAAATCTGCTCAAGAAGCGGATAGAAAGCGATGCGTGCGAATCGGGAGCGCG	3266
QY	3541	ATACCGTTAAGCACAGGAGCGGTGAGCCCATTTCCGCGCAAGCTCTTCAGCAATATCA	3600
Db	3267	ATACCGTTAAGCACAGGAGCGGTGAGCCCATTTCCGCGCAAGCTCTTCAGCAATATCA	3326
QY	3601	CGGTTAGCCAAACGCTATGCTCATAGCGGTCCGCGCACACCCAGCCGCGCACAGTCGATG	3660
Db	3327	CGGTTAGCCAAACGCTATGCTCATAGCGGTCCGCGCACACCCAGCCGCGCACAGTCGATG	3386
QY	3661	AATCCAGAAAGCGGCGCATTTTCCACATGATATTCCGCAAGCAGGCAATCGCCATGGGT	3720
Db	3387	AATCCAGAAAGCGGCGCATTTTCCACATGATATTCCGCAAGCAGGCAATCGCCATGGGT	3446
QY	3721	ACGACGAGATCTTCGCGGTGCGGCGATGCTCGCTTCAGCTTCGCAACAGTTCGGCTGGC	3780
Db	3447	ACGACGAGATCTTCGCGGTGCGGCGATGCTCGCTTCAGCTTCGCAACAGTTCGGCTGGC	3506
QY	3781	GCGAGCCCTTGATGCTCTTCGTCAGATCATCTGATCGAAGACCGGCTTCATCCGA	3840
Db	3507	GCGAGCCCTTGATGCTCTTCGTCAGATCATCTGATCGAAGACCGGCTTCATCCGA	3566
QY	3841	GTAAGTCTGCTCGATGCGATGTTTCGCTTGTGTGTGTAATGGGCAAGGTAGCGGATCA	3900
Db	3567	GTAAGTCTGCTCGATGCGATGTTTCGCTTGTGTGTGTAATGGGCAAGGTAGCGGATCA	3626
QY	3901	AGGTTATGACGCGCGCATTTGATCAGCCATCATGATATTTCTCGGAGGAGCAAGG	3960
Db	3627	AGGTTATGACGCGCGCATTTGATCAGCCATCATGATATTTCTCGGAGGAGCAAGG	3686
QY	3961	TGAGATGACAGGAGATCTTCGCGCGCATTTCCGCCCAATAGCAGCCAGTCCCTTCCGCT	4020
Db	3687	TGAGATGACAGGAGATCTTCGCGCGCATTTCCGCCCAATAGCAGCCAGTCCCTTCCGCT	3746
QY	4021	TCAGTCAACAGCTGAGACAGCTGCGCAAGGAACCGCGCTGCTGCGCAGCAGATAGC	4080
Db	3747	TCAGTCAACAGCTGAGACAGCTGCGCAAGGAACCGCGCTGCTGCGCAGCAGATAGC	3806
QY	4081	CGGCTGCTCTGCTTTCAGTTTCATTTCAGGGCACCGGACAGTTCGCTTTGACAAAAGA	4140
Db	3807	CGGCTGCTCTGCTTTCAGTTTCATTTCAGGGCACCGGACAGTTCGCTTTGACAAAAGA	3866
QY	4141	ACCGGCGCGCTTCGCTGACAGCGGAAACAGCGCGCATCAGAGCAGCGGATTTGTCTGT	4200
Db	3867	ACCGGCGCGCTTCGCTGACAGCGGAAACAGCGCGCATCAGAGCAGCGGATTTGTCTGT	3926
QY	4201	TGTGCGGCTCATAGCCGAATAGCTCTCCACCAAGCGCGGAGAACCTGCTGCAAT	4260
Db	3927	TGTGCGGCTCATAGCCGAATAGCTCTCCACCAAGCGCGGAGAACCTGCTGCAAT	3986
QY	4261	CCATCTGTTTCAATCATGCGAAACGATCTCTATCTCTCTCTTGTATCAGAGCTTGATCCC	4320
Db	3987	CCATCTGTTTCAATCATGCGAAACGATCTCTATCTCTCTCTTGTATCAGAGCTTGATCCC	4046
QY	4321	CTGCGCCATCAG 4332	

```
Db      |||||||
4047 CTGGCCATCAG 4058

RESULT 5
ADT55137
ID      ADT55137 standard; DNA; 5753 BP.
XX
AC      ADT55137;
XX
DT      30-DEC-2004 (first entry)
XX
DE      Nucleotide sequene of expression vector pMB1-Catalase.
XX
KW      Ophthalmological; radiation; free radical; superoxide anion;
KW      heavy metal cation; metallothionein; superoxide dismutase; SOD; catalase;
KW      glutathione peroxidase 4; Gpx-4; gamma glutamyl transpeptidase;
KW      xerostomia; xerophthalmia; autoimmune disorder; Sjogren's syndrome;
KW      graft-versus-host disease; systemic lupus erythematosus;
KW      rheumatoid arthritis; HIV-1 infection; ageing; autonomic dysfunction;
KW      psychogenic disorder; trauma; hepatitis C; cancer; mastication; ss.
XX
OS      Homo sapiens.
OS      Simian virus 40.
OS      Synthetic.
XX
FH      Key
CDS      Location/Qualifiers
FT      11..2270
FT      /*tag= a
FT      /note= "human catalase cDNA"
FT      332..497
FT      intron
FT      /*tag= b
FT      /note= "human beta-globin intron"
FT      347..503
FT      polyA_signal
FT      /*tag= c
FT      /note= "SV40 late gene polyadenylation signal"
FT      471..1162
FT      promoter
FT      /*tag= d
FT      /note= "CMV promoter"
FT      1158..1825
FT      rep_origin
FT      /*tag= e
FT      /note= "ColE1 ori from pBluescript SK-"
FT      1226..2020
FT      CDS
FT      /*tag= f
FT      /gene= "kanamycin resistance gene"
XX
PN      WO2004087873-A2.
XX
PD      14-OCT-2004.
XX
PF      26-MAR-2004; 2004WO-US009194.
XX
PR      26-MAR-2003; 2003US-0458793P.
PR      25-MAR-2004; 2004US-07778889.
XX
PA      (GENT-) GENTERIC INC.
XX
PI      Bennett MJ, Chen Y;
XX
DR      WPI; 2004-737685/72.
XX
PT      Attenuating increases in concentrations of radiation-induced free
PT      radicals in a mammalian cell, comprises contacting the cell with one or
PT      more nucleic acids encoding proteins that neutralizes or eliminates a
PT      portion of free radicals.
XX
PS      Claim 34; SEQ ID NO 3; 58pp; English.
XX
CC      The specification describes a method for attenuating increases in
CC      concentrations of radiation-induced free radicals, superoxide anions or
CC      heavy metal cations in a mammalian cell. The method comprises contacting
CC      the cell with one or more nucleic acids encoding one or more proteins
CC      that are expressed in the cell and that neutralizes or eliminates a
```

```
CC      portion of the free radicals, superoxide anions or heavy metal cations in
CC      the cell. The proteins are selected from metallothionein, superoxide
CC      dismutase, catalase, glutathione peroxidase (Gpx)-4, or gamma glutamyl
CC      transpeptidase. The method is useful for attenuating increases in
CC      concentrations of radiation-induced free radicals, superoxide anions or
CC      heavy metal cations in a mammalian cell, and ameliorating symptoms of
CC      xerostomia or xerophthalmia associated with conditions such as autoimmune
CC      disorders, Sjogren's syndrome, graft-versus-host disease, systemic lupus
CC      erythematosus, rheumatoid arthritis, HIV-1 infection, ageing, autonomic
CC      dysfunction, conditions affecting the CNS, psychogenic disorder, trauma,
CC      hepatitis C, cancer and decrease in mastication. The present sequence
CC      represents an expression vector used in the method of the invention to
CC      express the relevant proteins.
XX
SQ      Sequence 5753 BP; 1479 A; 1416 C; 1418 G; 1440 T; 0 U; 0 Other;
      Query Match      54.1%; Score 2341.8; DB 13; Length 5753;
      Best Local Similarity 99.4%; Pred. No. 2.6e-248;
      Matches 2349; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY      1971 AAAAAAAAAAAAAACGGAAATCCCTGCAGCCCGGGGATCCACTAGTTCTTAGAGCGGC 2030
DB      |||||||
QY      3392 ACAATAAATAATCTGTACGGAATTCCTGCAGCCCGGGGATCCACTAGTTCTTAGAGCGGC 3451
DB      |||||||
QY      2031 CGCCACCGGTGAGCTCCACAACACTAGATGCAAAAAAATGCTTTATTGTGAAA 2090
DB      |||||||
QY      3452 CGCCACCGGTGAGCTCCACAACACTAGATGCAAAAAAATGCTTTATTGTGAAA 3511
DB      |||||||
QY      2091 TTTGTGATGCTATTGCTTTATTGTAACCATTAAGCTGCAATAAACAAGTTAAACAACA 2150
DB      |||||||
QY      3512 TTTGTGATGCTATTGCTTTATTGTAACCATTAAGCTGCAATAAACAAGTTAAACAACA 3571
DB      |||||||
QY      2151 ATTGCATTCATTTATGTTTCAGGTTTTCAGGGGAGGTGTGGAGGTTTTTAAAGCCACA 2210
DB      |||||||
QY      3572 ATTGCATTCATTTATGTTTCAGGTTTTCAGGGGAGGTGTGGAGGTTTTTAAAGCCACA 3631
DB      |||||||
QY      2211 GCTCCAGCTTTGTTCCCTTTAGTTCAGGGTTAAATTCGAGCTGCGGTAATCATGTGCTAT 2270
DB      |||||||
QY      3632 GCTCCAGCTTTGTTCCCTTTAGTTCAGGGTTAAATTCGAGCTGCGGTAATCATGTGCTAT 3691
DB      |||||||
QY      2271 AGCTGTTTCTGTGTGAAATTTGTTATCCGCTCACAAATTCACACAACATACGAGCCGAA 2330
DB      |||||||
QY      3692 AGCTGTTTCTGTGTGAAATTTGTTATCCGCTCACAAATTCACACAACATACGAGCCGAA 3751
DB      |||||||
QY      2331 GCATAAAGTGAAGCCTGGGGTGCTTAATGAGTGAGCTTAATCATTAATTTGGTTCG 2390
DB      |||||||
QY      3752 GCATAAAGTGAAGCCTGGGGTGCTTAATGAGTGAGCTTAATCATTAATTTGGTTCG 3811
DB      |||||||
QY      2391 GCTCACTGCCGCTTTCCAGTCGGGAAACCTGTCGTGCGAGCTGCATTAATGAATCGGCC 2450
DB      |||||||
QY      3812 GCTCACTGCCGCTTTCCAGTCGGGAAACCTGTCGTGCGAGCTGCATTAATGAATCGGCC 3871
DB      |||||||
QY      2451 AACGCGCGGGAGAGCGGTTTGGCGTATTGGGCGCTCTTCCGCTTCTCGCTCACTGACT 2510
DB      |||||||
QY      3872 AACGCGCGGGAGAGCGGTTTGGCGTATTGGGCGCTCTTCCGCTTCTCGCTCACTGACT 3931
DB      |||||||
QY      2511 CGCTCGCTCGGTTCGTTCCGTCGCGGAGCGGTATCAGCTCACTCAAGGCGGTAATAC 2570
DB      |||||||
QY      3932 CGCTCGCTCGGTTCGTTCCGTCGCGGAGCGGTATCAGCTCACTCAAGGCGGTAATAC 3991
DB      |||||||
QY      2571 GGTATTACACAGAATCAGGGGATAACGAGGAAAGAAACATGTGAGCAAAAGGCCAGCAAA 2630
DB      |||||||
QY      3992 GGTATTACACAGATCAGGGGATAACGAGGAAAGAAACATGTGAGCAAAAGGCCAGCAAA 4051
DB      |||||||
QY      2631 AGGCCAGGAACCGTTAAAAAGCGCGGTGCTCGGCTTTTTCATAGGCTCCGCCCCCTG 2690
DB      |||||||
QY      4052 AGGCCAGGAACCGTTAAAAAGCGCGGTGCTCGGCTTTTTCATAGGCTCCGCCCCCTG 4111
DB      |||||||
QY      2691 ACAGCATCACAAAAATCGACCTCAAGTCAGAGTGGCGAAACCCGACAGACTATAAA 2750
DB      |||||||
QY      4112 ACAGCATCACAAAAATCGACCTCAAGTCAGAGTGGCGAAACCCGACAGACTATAAA 4171
DB      |||||||
QY      2751 GATACCAGGCGTTTCCCCCTGGAAAGCTCCCTCGTGGCTCTCTCTGTTCGACCCCTCCCGC 2810
```


FT	CDS	1173..3419	AGCTGTTTCTGTGTAATTTGTTATCCGCTCAAAATTCACACAAATACAGACCGGAA	2330
FT	FT	/*tag= f		
FT	FT	/note= "encodes catalase"		
FT	CDS	1226..2020	AGCTGTTTCTGTGTAATTTGTTATCCGCTCAAAATTCACACAAATACAGACCGGAA	3758
FT	FT	/*tag= g		
FT	FT	/gene= "kanamycin resistance gene"		
XX	WO2004087873-A2.		GCATAAGTGTAAAGCCTGGGGTGCCTAAATGAGTGAGCTAACTCACATTAATTGCGTTGC	2390
XX	XX			
XX	XX			
XX	XX			
XX	PD	14-OCT-2004.	GCTCACTGCCCGCTTTCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCC	2450
XX	XX			
XX	EF	26-MAR-2004; 2004WO-US009194.	GCTCACTGCCCGCTTTCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCC	3878
XX	XX			
XX	PR	26-MAR-2003; 2003US-0458793P.	AACGCGGGGAGAGCGGTTTGGGTATTCGGGCTCTTCCGCTTCTCGCTCACTGACT	2510
XX	PR	25-MAR-2004; 2004US-0777889.	AACGCGGGGAGAGCGGTTTGGGTATTCGGGCTCTTCCGCTTCTCGCTCACTGACT	3938
XX	PA	(GENT-) GENTERIC INC.		
XX	PI	Bennett MJ, Chen Y;	CGTCGCTCGGTCGTTTCGGCTGGCGGAGCGGTATCAGCTCACTCAAGGCGGTAATAC	2570
XX	DR	WPI; 2004-737685/72.		
XX	PT		CGTCGCTCGGTCGTTTCGGCTGGCGGAGCGGTATCAGCTCACTCAAGGCGGTAATAC	3998
XX	PT			
XX	PT		GGTTATCCACAGATCAGGGGATTAACGAGAAAGAAACATGTGAGCAAAAGGCGCAGCAA	2630
XX	PT			
XX	PT		GGTTATCCACAGATCAGGGGATTAACGAGAAAGAAACATGTGAGCAAAAGGCGCAGCAA	4058
XX	PT			
XX	PT		AGGCAGAAACCGTAAAGAAAGGCGGTTGCTGGCGTTTTCATAGGCTCCGCCCCCTG	2690
XX	PS	Claim 34; SEQ ID NO 4; 58pp; English.		
XX	XX		AGGCAGAAACCGTAAAGAAAGGCGGTTGCTGGCGTTTTCATAGGCTCCGCCCCCTG	4118
XX	CC			
XX	CC		ACGAGCATCAAAAATCGACGCTCAAGTCAGAGTGGCGGAAACCCGACGAGCTATAAA	2750
XX	CC			
XX	CC		ACGAGCATCAAAAATCGACGCTCAAGTCAGAGTGGCGGAAACCCGACGAGCTATAAA	4178
XX	CC			
XX	CC		GATACACAGGCTTTCCCGCTGGAAAGTCCCTCGTGGCGCTCTCTCTGTTCCGACCTCGCGC	2810
XX	CC			
XX	CC		GATACACAGGCTTTCCCGCTGGAAAGTCCCTCGTGGCGCTCTCTCTGTTCCGACCTCGCGC	4238
XX	CC			
XX	CC		TTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCAATGCTCAC	2870
XX	CC			
XX	CC		TTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCAATGCTCAC	4298
XX	CC			
XX	CC		GCTGTAGTATCTCAGTTCGGTGTAGTTCGCTCAAGCTGGGCTGTGTGACGAAAC	2930
XX	CC			
XX	CC		GCTGTAGTATCTCAGTTCGGTGTAGTTCGCTCAAGCTGGGCTGTGTGACGAAAC	4358
XX	CC			
XX	CC		CCCCGTTTACGCGGACCGCTTATCCGGTAACTATCGTCTTGAAGTCCAAACCCCG	2990
XX	CC			
XX	CC		CCCCGTTTACGCGGACCGCTTATCCGGTAACTATCGTCTTGAAGTCCAAACCCCG	4418
XX	SQ	Sequence 5760 BP; 1471 A; 1422 C; 1426 G; 1441 T; 0 U; 0 Other;		
XX	Query Match	54.1%; Score 2341.8; DB 13; Length 5760;	TAAGACAGCTTATCGCCACTGGCAGCAGCACTGGTAAACAGGATTAAGCAGAGGAGT	3050
XX	Best Local Similarity	99.4%; Pred. No. 2.6e-248;		
XX	Matches 2349; Conservative	0; Mismatches 13; Indels 0; Gaps 0;	TAAGACAGCTTATCGCCACTGGCAGCAGCACTGGTAAACAGGATTAAGCAGAGGAGT	4478
QY	1971	AAAAAAAAAAAAACGAATTCCTCGAGCCCGGGGATCCACTAGTTCTTAGAGCGGC	2030	
DB	3399	ACAAATAAATACTGTACGGAATTCCTGAGCCCGGGGATCCACTAGTTCTTAGAGCGGC	3458	
QY	2031	CGCCACCGGGTGGAGCTCCAACTAGAAATGCAAGTGAAGGAGGTTTATTTGTAAG	2090	
DB	3459	CGCCACCGGGTGGAGCTCCAACTAGAAATGCAAGTGAAGGAGGTTTATTTGTAAG	3518	
QY	2091	TTTGATGCTATTGCTTTATTTGTAACCAATTATAGCTGCAATAAAGTAAACA	2150	
DB	3519	TTTGATGCTATTGCTTTATTTGTAACCAATTATAGCTGCAATAAAGTAAACA	3578	
QY	2151	ATTGATTCATTTTATTTGTTTACGTTTACGGGGAGGTGGGAGGTTTATTTGTAAG	2210	
DB	3579	ATTGATTCATTTTATTTGTTTACGTTTACGGGGAGGTGGGAGGTTTATTTGTAAG	3638	
QY	2211	GCTCCAGCTTTTGTCCCTTTATGAGGGTTAATTTGAGCTTGGCGTAAATCATGTCAT	2270	
DB	3639	GCTCCAGCTTTTGTCCCTTTATGAGGGTTAATTTGAGCTTGGCGTAAATCATGTCAT	3698	

QY 3351 GTATTAGAAATAAACAATAGGGGTTCCGCGACATTTCCCGGAAAGTGCACCTG 3410
 Db 4779 GTAATTTAGAAAAATAAACAATAGGGGTTCCGCGACATTTCCCGGAAAGTGCACCTG 4838
 QY 3411 TATCGGTGTCAATACCGGACAGATCGGTAAGAGAAATAACCGCATCAGGAAATTGTA 3470
 Db 4839 TATCGGTGTCAATACCGGACAGATCGGTAAGAGAAATAACCGCATCAGGAAATTGTA 4898
 QY 3471 AGCGTTAATAATTCAGAAAGAACTCGTCAAGAAAGCGGATAGAAAGCGGATCGCTCGGAATC 3530
 Db 4899 AGCGTTAATAATTCAGAAAGAACTCGTCAAGAAAGCGGATAGAAAGCGGATCGCTCGGAATC 4958
 QY 3531 GGGAGCGCGATACCGTAAAGACACGAGAAAGCGGTACGCCCATTCGCGGCAAGCTCTTC 3590
 Db 4959 GGGAGCGCGATACCGTAAAGACACGAGAAAGCGGTACGCCCATTCGCGGCAAGCTCTTC 5018
 QY 3591 AGCAATATCAGGGTAGCCACGCTATGTCTGTATAGGGTCCGCGACACCCAGCCGGCC 3650
 Db 5019 AGCAATATCAGGGTAGCCACGCTATGTCTGTATAGGGTCCGCGACACCCAGCCGGCC 5078
 QY 3651 ACAGTCGATGAATCCAGAAAGCGGCCATTTTCCACCATGATATTCGCGAAGCAGGCATC 3710
 Db 5079 ACAGTCGATGAATCCAGAAAGCGGCCATTTTCCACCATGATATTCGCGAAGCAGGCATC 5138
 QY 3711 GCCATGGGTACGACGAGATCCTCGCGTGGGCGATCTCGCCTTGAGCCTTGCGGAACAG 3770
 Db 5139 GCCATGGGTACGACGAGATCCTCGCGTGGGCGATCTCGCCTTGAGCCTTGCGGAACAG 5198
 QY 3771 TTCGGCTGGCGGAGCCCTGATGCTCTTGTTCAGATCATCTCTGATCGACAGACCGGC 3830
 Db 5199 TTCGGCTGGCGGAGCCCTGATGCTCTTGTTCAGATCATCTCTGATCGACAGACCGGC 5258
 QY 3831 TTCATCCGAGTACGCTCGCTCGATGCGATGTTTCGTTGGTGGTTCGATGCGAGGT 3890
 Db 5259 TTCATCCGAGTACGCTCGCTCGATGCGATGTTTCGTTGGTGGTTCGATGCGAGGT 5318
 QY 3891 AGCCGATCAAGCGTATGCAAGCCCGCATTCGATCAGCCATGATGATATCTTCTCGGC 3950
 Db 5319 AGCCGATCAAGCGTATGCAAGCCCGCATTCGATCAGCCATGATGATATCTTCTCGGC 5378
 QY 3951 AGGAGCAAGTGATGATCAGAGGATCCTGCCCCGCACTTCGCCCAATAGCAGCAGTC 4010
 Db 5379 AGGAGCAAGTGATGATCAGAGGATCCTGCCCCGCACTTCGCCCAATAGCAGCAGTC 5438
 QY 4011 CTTTCCCGCTTCAGTGACCAAGCTCGAGCAGAGCTGCGCAAGGACGCCCTCGTGCCAG 4070
 Db 5439 CTTTCCCGCTTCAGTGACCAAGCTCGAGCAGAGCTGCGCAAGGACGCCCTCGTGCCAG 5498
 QY 4071 CCACGATAGCGCGCTCGCTGCTTGTGAGTTTCAATCAGGGCACCGGACAGGTGCGTCT 4130
 Db 5499 CCACGATAGCGCGCTCGCTGCTTGTGAGTTTCAATCAGGGCACCGGACAGGTGCGTCT 5558
 QY 4131 GACAAAAGAACCGGCGCCCTCGCTGACGCGGAAACCGGCGCATCAGAGCAGCC 4190
 Db 5559 GACAAAAGAACCGGCGCCCTCGCTGACGCGGAAACCGGCGCATCAGAGCAGCC 5618
 QY 4191 GATTGTCTGTGTGCCAGTCATAGCCGAATAGCTCTCCACCCAAAGCGCGCGAGAAC 4250
 Db 5619 GATTGTCTGTGTGCCAGTCATAGCCGAATAGCTCTCCACCCAAAGCGCGCGAGAAC 5678
 QY 4251 TGGGTCAATCCATCTTTGTTCAATCATGCGAAACGATCCTCTCTCTTTGATCAGA 4310
 Db 5679 TGGGTCAATCCATCTTTGTTCAATCATGCGAAACGATCCTCTCTCTTTGATCAGA 5738
 QY 4311 GCTTGATCCCTCGCCATCAG 4332
 Db 5739 GCTTGATCCCTCGCCATCAG 5760

RESULT 7

AAI70085

ID AAI70085 standard; DNA; 3609 BP.

XX

AAI70085;
 AC
 XX 11-SEP-2003 (revised)
 DT 21-DEC-2001 (first entry)
 XX
 DE Plasmid pPEI403 encoding mouse erythropoietin.
 XX
 KW Plasmid pPEI403; erythropoietin; mouse; gene delivery; anaemia;
 KW gene therapy; vaccine; ds.
 XX
 OS Homo sapiens.
 OS Human herpesvirus 5.
 OS Chimeric.
 XX
 PH Key Location/Qualifiers
 FT CDS 801..1379
 FT /*tag= a
 FT /product= "mouse erythropoietin"
 XX
 PN WO200166149-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 02-MAR-2001; 2001WO-US006953.
 XX
 PR 03-MAR-2000; 2000US-0187236P.
 PR 16-JAN-2001; 2001US-0261751P.
 XX
 PA (VALE-) VALENTIS INC.
 XX
 PI Fewell JG, MacLaughlin F, Smith LC, Nicol F, Rolland A;
 XX
 XX WPI; 2001-638995/73.
 DR
 XX
 PT Nucleic acid formulation for gene delivery to a muscle or tumor tissue to
 PT treat cancer, or infectious disease in a mammal, comprises a nucleic acid
 PT and non-encapsulating anionic polymer such as poly-L-glutamate.
 XX
 PS Example 4; Page 90-91; 98pp; English.
 XX
 CC The present sequence is that of expression plasmid pPEI403, which encodes
 CC mouse erythropoietin (EPO). The IFN-alpha coding sequence was inserted
 CC into the Valenti plasmid backbone containing a 107 bp 5' untranslated
 CC region, a 117 bp synthetic intron, the human growth hormone
 CC polyadenylation signal, a pUC12 origin of replication and a kanamycin
 CC resistance gene, such that the EPO gene was driven by the cytomegalovirus
 CC enhancer/promoter. The resulting plasmid, pPEI403, was formulated with
 CC poly-L-glutamate to produce a gene delivery vehicle, which was
 CC intramuscularly injected into mice, under electroporation conditions.
 CC Delivery of the plasmid DNA in the poly-glutamate formulation resulted in
 CC considerably higher levels of expressed protein than when the plasmid DNA
 CC was delivered in saline. This is an example of a method designed for non-
 CC viral plasmid-based gene therapy. In this method, a nucleic acid is
 CC formulated with a non-encapsulating anionic polymer, such as
 CC (biodegradable) poly-L-glutamate, which enhances transfection of the
 CC nucleic acid into muscle or tumour tissues, with or without
 CC electroporation, and which also stabilises the nucleic acid during
 CC storage. The formulations allow for vaccination and treatment of muscle
 CC disorders and serum protein deficiencies, as well as cancer and
 CC infections. In the case of EPO gene delivery, it may be used to treat
 CC anaemia. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 3609 BP; 811 A; 1031 C; 953 G; 814 T; 0 U; 0 Other;

Query Match 44.7%; Score 1937; DB 5; Length 3609;
 Best Local Similarity 72.1%; Pred. NO. 5.9e-204;
 Matches 2894; Conservative 0; Mismatches 626; Indels 492; Gaps 9;

QY 321 CGTTACATAACTTACGGTAAATGGCCGCTGCTGACCGCCCAAGACCCCCGCCCATTT 380

Db 26 CGTTACATAACTTACGGTAAATGGCCGCTGCTGACCGCCCAAGACCCCCGCCCATTT 85

QY 381 GACGTCAATTAAGACGTATGTTCCCAATAGTAACGCCCAATAGGAGCTTTCCATTGACGTCA 440

Db 86 GACGTCAATATGACGTATGTTCCATAGTAACGCCAATAGGACCTTCCATTGACGTCA 145
 Qy 441 ATGGGTGAGTATTTACGGTAAATGCGCCACTTGGCAGTACATCAAGTGTATCATATGCC 500
 Db 146 ATGGGTGAGTATTTACGGTAAATGCGCCACTTGGCAGTACATCAAGTGTATCATATGCC 205
 Qy 501 AAGTACGCCCTTATGACGTCAATGACGGTAAATGCGCCCTGGCATTATGCCAGTA 560
 Db 206 AAGTACGCCCTTATGACGTCAATGACGGTAAATGCGCCCTGGCATTATGCCAGTA 265
 Qy 561 CATGACCTTATGGGACTTTCTTCTATGGCAGTACATCTACGATATAGTATCGCTATATAC 620
 Db 266 CATGACCTTATGGGACTTTCTTCTATGGCAGTACATCTACGATATAGTATCGCTATATAC 325
 Qy 621 CATGGTATGGGTTTGGCAGTACATCAATGGGGTGGATAGCGTTTGAAGTCAACGGGG 680
 Db 326 CATGGTATGGGTTTGGCAGTACATCAATGGGGTGGATAGCGTTTGAAGTCAACGGGG 385
 Qy 681 ATTTCCAAAGTCTCCACCCCAATGACGTCAATGGGAGTTTGTGGCACCACCAAAATCAACG 740
 Db 386 ATTTCCAAAGTCTCCACCCCAATGACGTCAATGGGAGTTTGTGGCACCACCAAAATCAACG 445
 Qy 741 GACATTTCCAAATGCTGTAAACAACTCCGCCCATTTGACGCAATGACGCAATGGCGGTAGCGTGT 800
 Db 446 GACATTTCCAAATGCTGTAAACAACTCCGCCCATTTGACGCAATGACGCAATGGCGGTAGCGTGT 505
 Qy 801 ACGGTGGAGTCTATATAGCAGAGCTCGTTTGTAGTGAACGCTGAGATCGCTGGAGACG 860
 Db 506 ACGGTGGAGTCTATATAGCAGAGCTCGTTTGTAGTGAACGCTGAGATCGCTGGAGACG 565
 Qy 861 CCATCCACGCTGTTTGTGACCTCCATAGAGACACCGGACCGCATCCAGCTGACTCTAGC 920
 Db 566 CCATCCACGCTGTTTGTGACCTCCATAGAGACACCGGACCGCATCCAGCTCCCGGGCCG 625
 Qy 921 CTAGCTCTGAAGTGGTGTAGGCGCTCGGGCAGGTGGTATCAAGGTTACAGACAGGT 980
 Db 626 GGAACGGTGCATTGGAACGCG----- 646
 Qy 981 TTAAGGAGACCAATAGAACTGGGATGAGAGACAGAAAGACTCTTGGGTTCTGATA 1040
 Db 647 -----GATTCCCGGTGTTAATTAACAGGTAGTGTCTTCTCTCTGTTCC 691
 Qy 1041 GGCACTGACTCTCTGCTGCTATGTTCTATTTTCCACCCCTTAGCTGCTGCTGAGCC 1100
 Db 692 TTTCCCTGCTATTTCTGCTCAACCTTCTATCAGAACTGCACTATCTGTAATTTGCTAG 751
 Qy 1101 TAGGAGATCTCTGAGGTGACGCTATCGATAAGCTTGATGATCGAATTCGGGCGCGCA 1160
 Db 752 CAGTAATACTAACGGTCTCTTTTCTCTTCAAGGCCACCAAGCTTCCATGGGGTGCC 811
 Qy 1161 GGAGCGGCACTCGTGGCTGTGGCTTCGGCAGCGGCTTCAGCAGATCGCGGGCATCAG 1220
 Db 812 CGAAAGCCCCACCTGCTGCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
 Qy 1221 CGGTAGCACAGCAGTATGAGCAGTATGAGCCGGCAGTGTGCGGACCAAGCAGCAGCT 1280
 Db 872 CCTCTGTGCTCCGCCACCTCATCTCGACAGTGGGTGCTGGAGAGGTATCATCTGGA 931
 Qy 1281 GGTCCGGTTTGGGGTATCTGGGCTCAGGCAAGCAGCAGCTCCCGACCTCCCTTA 1340
 Db 932 GGCCAAAG-----AGGCAGAAATGTCAACGATGGGTTGTGAGAA 971
 Qy 1341 CGACTACGGCGCCCTGGAACCTCAATCAACGGCGCAGATCATGCACTGCAACCAAGCA 1400
 Db 972 GGTCCAGACTGAGTGAAA----- 990
 Qy 1401 GCACCAAGCGGCTTACGTGAACAACTGAAACGTCACGAGGAGAAATCAAGAGCGGTT 1460
 Db 991 --ATATTACAGTCCCAAGATACCAAGTCAACTTCTATGCTTGGAAAGAAATGGAGGTGA 1048
 Qy 1461 GGCCAGGGAGATGTTACAGCCAGATAGCTCTTACAGCTGCACTCAAGTTCATGCTGG 1520

Db 1049 AGAACAGG-----CCATCGAAGTGTGGCAAGGCCCTGTCCCTGTCTCAGCGAAGCCATCCTGC 1104
 Qy 1521 TGGTCAATCAATCATAGCATTTTCTGGACAAACCTCAGCCCTAAACGGTGGTGGAGAAC 1580
 Db 1105 AGGCCAGGCCCTGCTGCGCAATTTCTCCAGCCACAGAGACCCCTCAGCTGCATATCG 1164
 Qy 1581 CAAAGGGGAGTGTGGAAGCCATCAAAACGTGACTTTGGTTCCTTTGACAAAGTTAAGGA 1640
 Db 1165 ACRAAGCCATCAGTGGTCTGC----- 1185
 Qy 1641 GAAGCTCAGCGCTGCATCTGTTGGTGTCCAAGGCTCAGGTTGGGTTGGCTTGGTTTCAA 1700
 Db 1186 -----GCAGCTCACTTCCCTGCTGCGGGTCTGGAGCTCAG 1223
 Qy 1701 TAAGGAACGGGGAACATTAACAAATGCTGTGTTGCCAAATCAGGATCCATGCAAGGAAC 1760
 Db 1224 AAGGAACGTGATGCTCCCTCCAGAT----- 1247
 Qy 1761 AACAGGCTTATTCACCTGCTGGGATGATGTGGGAGCAGCTTACTTACTTCACTTCA 1820
 Db 1248 -----ACCACCCCACTCTCCACTCC 1269
 Qy 1821 TAAAAATGTCAGGCTGATTATCTAAAGCTTATTTGGAATGTAATCAACTGGGAGATG 1880
 Db 1270 GCACACTCAGCTGATATCTTCTGCAAGCTCTTCCGGTCTACGCCA----- 1317
 Qy 1881 TAACGAAAGATACATGGCTTGCAAAAGTAAACCAAGATCGTTATGCTGTAAGAAAAA 1940
 Db 1318 -----ACTTCTCCGGGGAAACTGAAGCTGTACACGGGAGAGGTCTG 1360
 Qy 1941 AAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2000
 Db 1361 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1404
 Qy 2001 GCGCGGGGATCCACTAGTCTTAGAGCGCGCCACCGCGGTGGAGCTCCCAACTAGAA 2060
 Db 1405 AATTGGGTGGCATCCCTGTGACCCCTCCCAAGTGCCTCTCGGCCCTGGAGGTTGCCAC 1464
 Qy 2061 TGCAAGTAAAAAATGCTTATTTGTGAAATTTGTGATGCTTATGCTTATTTGTAACA 2120
 Db 1465 TCCAGTGCCACAGCCCTGTCTTAATAAATTAAGTTGTCATCAATTTGTCTGACTAGT 1524
 Qy 2121 TTAAGCTGCAATAAACAAGTAAACAATTCATTTATTTATGTTTTCAGGTTTCAGG 2180
 Db 1525 GTCCTTCTATATATATATGAGGGTGGAGGGGGTGTATGGAGCAAGGGGAGGTTGGGA 1584
 Qy 2181 GGGAGGTGTGGAGGTTTTTTAAAGCCACAGCTCCAGCTTTTGTTCCTTTAGTCAAGGT 2240
 Db 1585 GACAACTGTAGGCTCGAGGGGGGCGCGGTACCAGCTTTTGTTCCTTTAGTCAAGGT 1644
 Qy 2241 TAAATTCAGCTTGGCGTAATCAATGTCATAGCTGTTTCTGTGTGAAATTTGTTATCCGC 2300
 Db 1645 TAAATTCAGCTTGGCGTAATCAATGTCATAGCTGTTTCTGTGTGAAATTTGTTATCCGC 1704
 Qy 2301 TCACAAATTCACACAAATACAGCCGGAAGCATAAAGTGAAGCTTGGGTTGCTTAA 2360
 Db 1705 TCACAAATTCACACAAATACAGCCGGAAGCATAAAGTGAAGCTTGGGTTGCTTAA 1764
 Qy 2361 GAGTCAAGCTTAACTCACTTAAATTTGCGTCTCATCTGCCCTTTTCCAGTCCGGAAC 2420
 Db 1765 GAGTCAAGCTTAACTCACTTAAATTTGCGTCTCATCTGCCCTTTTCCAGTCCGGAAC 1824
 Qy 2421 TGTGTCAGCTGATGATTAATGAATCGGCAACCGCGGGGAGGCGGTTTGCCTATG 2480
 Db 1825 TGTGTCAGCTGATGATTAATGAATCGGCAACCGCGGGGAGGCGGTTTGCCTATG 1884
 Qy 2481 GCGCTCTTCCGCTTCTCGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2540
 Db 1885 GCGCTCTTCCGCTTCTCGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1944
 Qy 2541 CGGTATCAGCTCACTCAAGGGCGGTAATACGGTTATTCACAGATCAGGGGATTAACGAG 2600
 Db 1945 CGGTATCAGCTCACTCAAGGGCGGTAATACGGTTATTCACAGATCAGGGGATTAACGAG 2004

1231	AGAAGAAATACAGCCCTTGTGCTGGAGGTTGTGCAGAGCAGAAATCATGAGATCTTTTT	1299
Qy	GTAACTGAAGATACATGGCTTGCAAAAAGTAAACCAAGATCGTTATGCTGGAAAAAAA	1939
Db	CTTTGTC-----A	1298
Qy	AAACGGATTCCTCGC	1999
Db	ACAACTTGCAAGAAAGTTTAAAGATGAAGATCTAGAAAAAGCCGAATTCGCG	1358
Qy	AGCCCGGGGATCCACTAGTTCTTAGAGCGCGCACCGCGTGGAGCTCCACAACCTAGA	2059
Db	GAATTGGGTGCATCCCTGTGACCCCTCCCAAGTCCTCTCTCGCCCTGGAAGTTCGA	1418
Qy	ATGCAGTGA AAAAATGCTTTATTTGTGAAATTTGTGATGCTATGCTTTATTTGTGAACC	2119
Db	CTCAGTGGCCACAGCGCTTGCTCAATAAAATTAAGTTGCATCATTTTGTCTGACTAGG	1478
Qy	ATTATAAGCTCAATAAACAAAGTTAAACAAATTGCAATCATTTATGTTTTCAGTTTCAG	2179
Db	TGTCCTCTTATAATTTATGCGGTGGAGGGGTGGTATGGAGCAAGGCAAGTTGGGA	1538
Qy	GGGAGGTGTGGAGGTTTTTTAAAGCCAAGCTCCAGCTTTTGTTCCTTTTGTGAGGG	2239
Db	AGACAACCTGTAGGGCTCGAGGGGGGCGCGGTACCAAGCTTTTGTTCCTTTTGTGAGGG	1598
Qy	TTAATTTTCGAGCTTGGCGTAAATCATGTCTCATAGCTGTTTCTCTGTGTGAAATTTGTTATCCG	2299
Db	TTAATTTTCGAGCTTGGCGTAAATCATGTCTCATAGCTGTTTCTCTGTGTGAAATTTGTTATCCG	1658
Qy	CTCAATTTCCACAACAACATACGAGCGGAGCAATAAGTTAAAGCTTCGGGTGCCTAA	2359
Db	CTCAATTTCCACAACAACATACGAGCGGAGCAATAAGTTAAAGCTTCGGGTGCCTAA	1718
Qy	TGAGTGAGCTAACTCAATTAATTCGTTGGGCTCACTGCGCGCTTTCAGTTCGGGAAC	2419
Db	TGAGTGAGCTAACTCAATTAATTCGTTGGGCTCACTGCGCGCTTTCAGTTCGGGAAC	1778
Qy	CTGTCTGTGCAGCTGCATTAATGAATCGGCCAACCGCGCGGGAGAGCGGTTTTCGCTATT	2479
Db	CTGTCTGTGCAGCTGCATTAATGAATCGGCCAACCGCGCGGGAGAGCGGTTTTCGCTATT	1838
Qy	GGGCGCTTTCGCTTCTCGCTCACTGACTCGCTGCGCTCGGTCGTTGCGCTCGCGCGA	2539
Db	GGGCGCTTTCGCTTCTCGCTCACTGACTCGCTGCGCTCGGTCGTTGCGCTCGCGCGA	1898
Qy	CGCGTATCAGCTCACTCAAAAGGCGTAATACGGTTATCCACAGAAATCAGGGGATACGCA	2599
Db	CGCGTATCAGCTCACTCAAAAGGCGTAATACGGTTATCCACAGAAATCAGGGGATACGCA	1958
Qy	GGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGAACCTGAAAAAGGCCGGTTG	2659
Db	GGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGAACCTGAAAAAGGCCGGTTG	2018
Qy	CTGGGTTTTTCCATAGGCTTCGCCCCCTTGAAGAGCATCACAAAATCGACGCTCAAGT	2719
Db	CTGGGTTTTTCCATAGGCTTCGCCCCCTTGAAGAGCATCACAAAATCGACGCTCAAGT	2078
Qy	CAGAGTGGGGAACCCCGACGAGCTATAAGATACACAGCGCTTTCGCCCTGGAAGCTCC	2779
Db	CAGAGTGGGGAACCCCGACGAGCTATAAGATACACAGCGCTTTCGCCCTGGAAGCTCC	2138
Qy	CTGTGGGCTCTCTGTTTCGACCTGCGCGTTACCGGATACCTGTGCGGCTTTCTCCCT	2839
Db	CTGTGGGCTCTCTGTTTCGACCTGCGCGTTACCGGATACCTGTGCGGCTTTCTCCCT	2198
Qy	TCGGGAAGCGTGGCGCTTTCTCAATGCTCAGCGTGTAGGTATCTCAGTTTCGGTGTAGGTC	2899
Db	TCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCGTGTAGGTATCTCAGTTTCGGTGTAGGTC	2258
Qy	GTTCGCTCCAAAGCTGGGCTGTGTGACGAACCCCGGTTTCAGCCGACCGCTCGCGCTTA	2959
Db	GTTCGCTCCAAAGCTGGGCTGTGTGACGAACCCCGGTTTCAGCCGACCGCTCGCGCTTA	2318

QY 4040 CAGCTGGCGAAGAAACGCGCGTCTGGTGGCCAGCCACGATAGCCGCGCTCGCTCTTGCA 4099
 DB 3208 CAGCTGGCGAAGAAACGCGCGTCTGGTGGCCAGCCACGATAGCCGCGCTCGCTCTTGCA 3267
 QY 4100 GTTCATTACAGGCAACCGGACAGTGGTCTTGAACAAAAGAACCGGGCGGCCCTGGCGCTG 4159
 DB 3268 GTTCATTACAGGCAACCGGACAGTGGTCTTGAACAAAAGAACCGGGCGGCCCTGGCGCTG 3327
 QY 4160 ACAGCCGGAACACGCGCGCATCAGACGAGCGGATGCTGTGTGCGCCAGTCATAGCCGA 4219
 DB 3328 ACAGCCGGAACACGCGCGCATCAGACGAGCGGATGCTGTGTGCGCCAGTCATAGCCGA 3387
 QY 4220 ATAGCCTCTCCACCAAGCGCGGAGAACCTGGTGCATCTTGTTCATATGCG 4279
 DB 3388 ATAGCCTCTCCACCAAGCGCGGAGAACCTGGTGCATCTTGTTCATATGCG 3447
 QY 4280 GAAACGATCCTCATCTGCTCTTGTATCAGAGCTTGCCTGGCCATCAG 4332
 DB 3448 GAAACGATCCTCATCTGCTCTTGTATCAGATCTTGATCCCTCGGCCATCAG 3500

RESULT 9

ID AA240418 standard; DNA; 3589 BP.
 AC AA240418;
 DX 15-FEB-2000 (first entry)

Plasmid pIF0921 containing human IFN- α sequence.

Wild type; human; interferon- α ; plasmid; cytomegalovirus; CMV;
 promoter; growth hormone; untranslated region; UTR; mammal; disease;
 cancer; intron; ss.

Synthetic.

WO9947678-A2.

23-SEP-1999.

12-MAR-1999; 99WO-US005394.

19-MAR-1998; 98US-0078654P.

(GENE-) GENEMEDICINE INC.

Nordstrom J, Pericle F, Rolland A, Ralston R;

WPI; 1999-562116/47.

New plasmids containing an interferon- α coding sequence, used for the treatment of a mammalian condition or disease, particularly cancer.

Disclosure; Fig 6; 137pp; English.

The invention relates to a novel plasmid comprising a cytomegalovirus (CMV) promoter transcriptionally linked with an interferon α (IFN- α) coding sequence, and a growth hormone 3'-untranslated region (UTR). This sequence represents the plasmid pIF0921 which contains the human interferon α (IFN- α) gene. The plasmids can be used for treating a mammalian condition or disease, particularly cancer

Sequence 3589 BP; 832 A; 983 C; 933 G; 841 T; 0 U; 0 Other;

Query Match 44.4%; Score 1923.8; DB 2; Length 3589;

Best Local Similarity 72.2%; Pred. No. 1.6e-202;

Matches 2897; Conservative 0; Mismatches 603; Indels 512; Gaps 10;

321 CGTTACATAACTACCGTAAATGGCCCGCTGGCTGACCGCCCAACGACCCCGCCCAATT 380

1 CGTTACATAACTACCGTAAATGGCCCGCTGGCTGACCGCCCAACGACCCCGCCCAATT 60

QY 381 GACGTCATAATGACGATGATCTTCCCATAGTAACGCCAATAGGACATTTTCCATTGACGTCA 440
 DB 61 GACGTCATAATGACGATGATCTTCCCATAGTAACGCCAATAGGACATTTTCCATTGACGTCA 120
 QY 441 ATGGGTGGAGTATTTACGGTAAACTGCCCATTTGGCAGTACATCAAGTGTATCATATGCC 500
 DB 121 ATGGGTGGAGTATTTACGGTAAACTGCCCATTTGGCAGTACATCAAGTGTATCATATGCC 180
 QY 501 AAGTACGCCCCCTTATGACGTCATGACGTAATGACGTAATGACGTAATGACGTAATGACGTA 560
 DB 181 AAGTACGCCCCCTTATGACGTCATGACGTAATGACGTAATGACGTAATGACGTAATGACGTA 240
 QY 561 CATGACCTTATGGACATTTTCTACTTGGCAGTACATCTAGTATTAGTATTAGTATTAGTATTAG 620
 DB 241 CATGACCTTATGGACATTTTCTACTTGGCAGTACATCTAGTATTAGTATTAGTATTAGTATTAG 300
 QY 621 CATGGTCATCGGTTTTTGGCAGTACATCAATGGCGCTGGATAGCGGTTTGACTCACCGGG 680
 DB 301 CATGGTCATCGGTTTTTGGCAGTACATCAATGGCGCTGGATAGCGGTTTGACTCACCGGG 360
 QY 681 ATTTCCAAAGTCTCCACCCCATTTGACGTCATGACGTAATGACGTAATGACGTAATGACGTA 740
 DB 361 ATTTCCAAAGTCTCCACCCCATTTGACGTCATGACGTAATGACGTAATGACGTAATGACGTA 420
 QY 741 GGACTTTCCAAATGTCGTAACAACTCGGCCCATTTGACGTAATGACGTAATGACGTAATGACGTA 800
 DB 421 GGACTTTCCAAATGTCGTAACAACTCGGCCCATTTGACGTAATGACGTAATGACGTAATGACGTA 480
 QY 801 ACGGTGGGAGTCTATATAAGCAGAGCTCGTTTTAGTGAACCGTCAGATCGCTCGGAGACG 860
 DB 481 ACGGTGGGAGTCTATATAAGCAGAGCTCGTTTTAGTGAACCGTCAGATCGCTCGGAGACG 540
 QY 861 CCATCCACGCTGTTTTGACCTTCCATAGAACACCGGAGACCGATCGACTCTAGC 920
 DB 541 CCATCCACGCTGTTTTGACCTTCCATAGAACACCGGAGACCGATCGACTCTAGC 589
 QY 921 CTAGCTCTGAAGTTGGTGGTGGGCGCTGGGCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 980
 DB 590 ---CTCGCGCGCGCGGAAACGGTGCAATGGAAACCGGATTCCTCGCTGTTAATTAACAGGT 645
 QY 981 TTAAGGAGACCAATAGAAACTGGGCATGTGGAGACAGAGAAAGACTCTTTGGGTTTCTGATA 1040
 DB 646 ----- 645
 QY 1041 GGCACGTGACTCTCTGCTGCTATTTGCTGCTATTTTCCACCTTAGCTCTGCTGCTGAGCC 1100
 DB 646 -----AAGTGTCTTCT 686
 QY 1101 TAGGAGATCTCTCGAGGTCGACGGTATCGATAAGCTTCATATCGAATTCGGGCGCGCA 1160
 DB 687 ACCTTCTCTATCAGAACTGCAGTATCTGTATTTTGTGCTAGCAGTATTAACGGTTCTT 746
 QY 1161 GGAGCGGCACTCGTGGCTGTGGTGGCTTGGCGAGCGGCTTCAAGCAGATCGGCGGATCAG 1220
 DB 747 TTTTCTCTTTCACAGGCCACCATGSCCTTGACTTGTCTTA-CTGGTGGCCCTCTCTGT 805
 QY 1221 CGGTAGACACGACACTAGCAGCATGTTGAGCGCGGAGTGTGGCGCAGCAGGACGAGT 1280
 DB 806 GCTCAGCTGCAAGTCAAGCTGCTCTGTGGGCTGTGATCTGCTCTAAACCCACAGC----- 860
 QY 1281 GGCTCCGGTTTGGGGTATCTGGGCTCCAGGCGAGAACACAGCCTCCCCAGCTGCCCTTA 1340
 DB 861 -----CTGGGTAGCAGGAGGACCTTGATGCTCTCTGGCAGC----- 896
 QY 1341 CGACTACGCGCGCTCGGAACCTCACAACGCGCAGATCAATGACGCTGCAACACAGCAA 1400
 DB 897 -----ATGAGGAGAACT 928
 QY 1401 GCACACCGGCGCTAGGTGAACAACTGAACTCACCAGGAGAGTACACGAGGCGCTT 1460
 DB 929 GCACAGACATGACTTTTGGATTTCCCGAGGAGAGTTTGGCAACCACTAGTTTCAAAAGCTGA 988
 QY 1461 GSCCAAGGAGATGTTACAGCCCGAGATAGCTCTTTCAGCCCTGCACTGAAGTTCAATGGTGG 1520

QY 3681 TTCCACCATGATATTTCGCAAGCAGGAGCATGCCATGGGTCAAGCAGAGATCCTCGCGTC 3740
 DB |||||
 QY 2849 TTCCACCATGATATTTCGCAAGCAGGAGCATGCCATGGGTCAAGCAGAGATCCTCGCGTC 2908
 DB |||||
 QY 3741 GGGGATGTCGCCCTTGAGCCTGGCGAACAGATTCGGCTGGCGGAGCCCTGATGCTCTTC 3800
 DB |||||
 QY 2909 GGGGATGTCGCCCTTGAGCCTGGCGAACAGATTCGGCTGGCGGAGCCCTGATGCTCTTC 2968
 DB |||||
 QY 3801 GTCCAGATCATCTTCATGACAGACGGCTTCATCCGAGTACGTGCTGCTCGATGCG 3860
 DB |||||
 QY 2969 GTCCAGATCATCTTCATGACAGACGGCTTCATCCGAGTACGTGCTGCTCGATGCG 3028
 DB |||||
 QY 3861 ATGTTTCGCTTGGTGGTGCATGGGAGGTAGCCGATCAAGCGGTATGACGCCCGCAT 3920
 DB |||||
 QY 3029 ATGTTTCGCTTGGTGGTGCATGGGAGGTAGCCGATCAAGCGGTATGACGCCCGCAT 3088
 DB |||||
 QY 3921 TGCATCAGCCATGATGGATATCTTCTCGGAGGAGCAAGGTGAGATGACAGGATCTTG 3980
 DB |||||
 QY 3089 TGCATCAGCCATGATGGATATCTTCTCGGAGGAGCAAGGTGAGATGACAGGATCTTG 3148
 DB |||||
 QY 3981 CCCGGCACTTCGCCCATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAAAGTGGAGCAC 4040
 DB |||||
 QY 3149 CCCGGCACTTCGCCCATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAAAGTGGAGCAC 3208
 DB |||||
 QY 4041 AGCTGCGCAAGGAACGCCCGTCTGGCCAGGACGATAGCCGCGTCTGCTCTTGCGAG 4100
 DB |||||
 QY 3209 AGCTGCGCAAGGAACGCCCGTCTGGCCAGGACGATAGCCGCGTCTGCTCTTGCGAG 3268
 DB |||||
 QY 4101 TTCAATCAGGGACCGGACAGGTGCGTCTTGACAAAGAAAGAACCGGGCCCTGGGCTGA 4160
 DB |||||
 QY 3269 TTCAATCAGGGACCGGACAGGTGCGTCTTGACAAAGAAAGAACCGGGCCCTGGGCTGA 3328
 DB |||||
 QY 4161 CAGCGGGAACCGGCGCATCAGACGCGGATTCGTTGTGTCGCCAGTCAATAGCCGAA 4220
 DB |||||
 QY 3329 CAGCGGGAACCGGCGCATCAGACGCGGATTCGTTGTGTCGCCAGTCAATAGCCGAA 3388
 DB |||||
 QY 4221 TAGCCTCTCCACCCAAAGCGCGGAGAACCTGCGTGCATCAATCTTGTTCATCATGCG 4280
 DB |||||
 QY 3389 TAGCCTCTCCACCCAAAGCGCGGAGAACCTGCGTGCATCAATCTTGTTCATCATGCG 3448
 DB |||||
 QY 4281 AAACGATCTCATCTCTCTCTTGTATCAGAGCTTGATCCCTGCGCCATCAG 4332
 DB |||||
 QY 3449 AAACGATCTCATCTCTCTCTTGTATCAGATCTTGATCCCTGCGCCATCAG 3500
 DB |||||

RESULT 10
 ADF77242
 ID ADF77242 standard; DNA; 3589 BP.
 XX
 AC ADF77242;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Human IPN pIF0921.
 XX
 KW ds; human; interferon alpha expression plasmid; tumour; IL-12.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US2003181405-A1.
 XX
 PD 25-SEP-2003.
 XX
 PF 29-APR-2002; 2002US-00136837.
 XX
 PR 12-MAR-1999; 99US-00268135.
 XX
 PA (NORD/) NORDSTROM J L.
 PA (PERI/) PERICLE F.
 PA (ROLL/) ROLLAND A.
 PA (RALS/) RALSTON R O.

XX Nordstrom JL, Pericle F, Rolland A, Ralston RO;
 PI WPI; 2004-020834/02.
 XX
 PT A mammalian interferon alpha expression plasmid is useful in gene therapy
 PT to deliver interferon alpha to cells to modulate tumor activity in the
 PT treatment of cancer.
 XX
 PS Disclosure; SEQ ID NO 4; 65pp; English.
 PS
 CC The invention relates to a mammalian interferon alpha expression plasmid,
 CC comprising a promoter and a synthetic 5' intron transcriptionally linked
 CC with an interferon alpha coding sequence and a 3' untranslated region.
 CC The mammalian interferon alpha expression plasmid is useful for treating
 CC tumour growth. The present sequence is used in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 3589 BP; 832 A; 983 C; 933 G; 841 T; 0 U; 0 Other;
 Query Match 44.4%; Score 1923.8; DB 12; Length 3589;
 Best Local Similarity 72.2%; Pred. No. 1.6e-202;
 Matches 2897; Conservative 0; Mismatches 603; Indels 512; Gaps 10;
 QY 321 CGTTACATAACTTACGTTAAATGCGCCCTGGCTGACCGCCCAACGACCCCGCCCAATT 380
 DB 1 CGTTACATAACTTACGTTAAATGCGCCCTGGCTGACCGCCCAACGACCCCGCCCAATT 60
 QY 381 GACGTCAATATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTTCCATTGACGTCA 440
 DB 61 GACGTCAATATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTTCCATTGACGTCA 120
 QY 441 ATGGGTGAGATTTTACGGTAAATGCGCCACTTGGCAGTACATCAAGTGTATCATATGCC 500
 DB 121 ATGGGTGAGATTTTACGGTAAATGCGCCACTTGGCAGTACATCAAGTGTATCATATGCC 180
 QY 501 AAGTACGCCCCCTATTGACGTCAATGACGTAAATGCGCCCTGGCAGTATGCCCAGTA 560
 DB 181 AAGTACGCCCCCTATTGACGTCAATGACGTAAATGCGCCCTGGCAGTATGCCCAGTA 240
 QY 561 CATGACCTTATGGGACTTTCTTCTTGGCAGTACATCTACGTATTAGTTCATGCTATTAC 620
 DB 241 CATGACCTTATGGGACTTTCTTCTTGGCAGTACATCTACGTATTAGTTCATGCTATTAC 300
 QY 621 CATGCTGATGCGGTTTGGCAGTACATCAATGCGGCTGATAGCGTTTGACTACGCGG 680
 DB 301 CATGCTGATGCGGTTTGGCAGTACATCAATGCGGCTGATAGCGTTTGACTACGCGG 360
 QY 681 ATTTCCAAAGTCTCCACCCCATTTGACGTCAATGGGAGTTTGTGTCGACCCCAAAATCAACG 740
 DB 361 ATTTCCAAAGTCTCCACCCCATTTGACGTCAATGGGAGTTTGTGTCGACCCCAAAATCAACG 420
 QY 741 GGACTTTTCCAAAATGCTGTAACAATCTCGCCCATTTGACGCAAAATGGGCGTAGCGGTG 800
 DB 421 GGACTTTTCCAAAATGCTGTAACAATCTCGCCCATTTGACGCAAAATGGGCGTAGCGGTG 480
 QY 801 ACGGTGGGAGGTCTATATAAGCAGAGTCGTTTGTAGAACCGTCAAGTCCCTGGAGAGC 860
 DB 481 ACGGTGGGAGGTCTATATAAGCAGAGTCGTTTGTAGAACCGTCAAGTCCCTGGAGAGC 540
 QY 861 CCATCCAGCTGTTTGGACCTCCATAGAGACACCGGGACCGATCCAGCTGACTCTAGC 920
 DB 541 CCATCCAGCTGTTTGGACCTCCATAGAGACACCGGGACCGATCCAGC----- 589
 QY 921 CTAGCTCTGAAGTTGCTGGTGGGCGCTTGGGAGGTGGTATCAAGTTACAGAGGT 980
 DB 590 ----CTCGCGCGCGGGAACGGTGCATTTGGAACCGGGATTCGCCCGTGTAAATTAACAGGT 645
 QY 981 TTAAGGAGACCAATAGAAACTGGGCATGTGGAGACAGAGACTCTTGGGTTTCTGATA 1040
 DB 646 ----- 645
 QY 1041 GGCAGTACTCTCTCTGCTCTATTGGTCTATTTTCCACCCCTTAGGCTGCTGGTCTGAGCC 1100

Db 10486 ATTCGCCCAAGCTCTTCAGCAATATACGGGTAGCAACGCTATGTCCTGATAGCGGT 10545
 Qy 3632 CCGCCACACCCAGCGGCCAGTCGATGATCCAGAAAGGGGCCATTTTCACCATGA 3691
 Db 10546 CCGCCACACCCAGCGGCCAGTCGATGATCCAGAAAGGGGCCATTTTCACCATGA 10605
 Qy 3692 TATTGGCAGCAGGCATCGCCATCGGTCACGACGAGATCCTCGCCGTCGGGCATGCTCG 3751
 Db 10606 TATTGGCAGCAGGCATCGCCATCGGTCACGACGAGATCCTCGCCGTCGGGCATGCTCG 10665
 Qy 3752 CTTGAGCTCGGCAAGTTGCGTGGCGGAGCCCTGATGCTCTTTCGTCAGATCAT 3811
 Db 10666 CTTGAGCTCGGCAAGTTGCGTGGCGGAGCCCTGATGCTCTTTCGTCAGATCAT 10725
 Qy 3812 CCTGATCAGACAGCCGCTTCCATCCGAGTACGTCGCTCGATGCGATGTTTCGCTT 3871
 Db 10726 CCTGATCAGACAGCCGCTTCCATCCGAGTACGTCGCTCGATGCGATGTTTCGCTT 10785
 Qy 3872 GGTGTCGAATGGGAGGTAGCGGATCAAGCGTATGACGCGCGCATTCATCAGCCA 3931
 Db 10786 GGTGTCGAATGGGAGGTAGCGGATCAAGCGTATGACGCGCGCATTCATCAGCCA 10845
 Qy 3932 TGATGGATACCTTCTCGCAGGAGCAAGGTGAGATGACAGAGATCCTGCCCGGCACTT 3991
 Db 10846 TGATGGATACCTTCTCGCAGGAGCAAGGTGAGATGACAGAGATCCTGCCCGGCACTT 10905
 Qy 3992 CGCCCAATAGCAGCAGCTTCCGCTTCCAGTACGTCGATGACGACGACGTCGCGCAAG 4051
 Db 10906 CGCCCAATAGCAGCAGCTTCCGCTTCCAGTACGTCGATGACGACGACGTCGCGCAAG 10965
 Qy 4052 GAACGCCGCTCGTGCCAGCAGCAGTACGCGCTGCTCTGTCGATTCATTCAGGG 4111
 Db 10966 GAACGCCGCTCGTGCCAGCAGCAGTACGCGCTGCTCTGTCGATTCATTCAGGG 11025
 Qy 4112 CACCGACAGTCGCTTGTGACAAAGAACCGGCGCCCTCGCTGACGCGGGAACA 4171
 Db 11026 CACCGACAGTCGCTTGTGACAAAGAACCGGCGCCCTCGCTGACGCGGGAACA 11085
 Qy 4172 CGCGGCAATCAGACAGCAGCTTGTGTCGTCGCTGATGACGAGATCCTGCTTCCCA 4231
 Db 11086 CGCGGCAATCAGACAGCAGCTTGTGTCGTCGCTGATGACGAGATCCTGCTTCCCA 11145
 Qy 4232 CCCAAGCGCGGAGAACCTCGCTGCAATCCATCTTGTTCATATGCGAAACGATCCTC 4291
 Db 11146 CCCAAGCGCGGAGAACCTCGCTGCAATCCATCTTGTTCATATGCGAAACGATCCTC 11205
 Qy 4292 ATCTGTCTTGTATCAGAGCTTGTATCCCTGCGGCATCAG 4332
 Db 11206 ATCTGTCTTGTATCAGAGCTTGTATCCCTGCGGCATCAG 11246

RESULT 13

AAV50427
 ID AAV50427 standard; DNA; 3600 BP.
 AC
 AC AAV50427;
 XX
 XX
 DT 26-OCT-1998 (first entry)
 XX
 DE Plasmid pIG0552 upper expected sequence nucleotides 1-3600.
 XX
 KW Human; IGF-1; insulin-like growth factor 1; urinary incontinence;
 KW gene therapy; neurotrophic factor; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FN W09833529-A1.
 XX
 PD 06-AUG-1998.
 XX
 PF 04-FEB-1998; 98WO-US002051.

XX PR 04-FEB-1997; 97US-0036862P.
 XX (GENE-) GENEMEDICINE INC.
 XX Coleman M;
 XX WPI; 1998-437184/37.
 XX
 PT Treatment of urinary incontinence - by delivering nucleic acid vector for
 PT expression of growth factor or neurotrophic factor in tissue(s).
 XX
 PS Disclosure; Page 103-105; 117pp; English.
 XX
 CC A method has been developed of treating urinary incontinence (UI) in
 CC mammals. The method comprises delivering a nucleic acid vector for the
 CC expression of a growth factor or neurotrophic factor in a tissue or
 CC tissues. The present sequence represents the expected upper sequence of
 CC plasmid pIG0552 nucleotides 1-3600 from the present invention. Due to the
 CC growth and stimulatory effects of growth factors and neurotrophic
 CC factors, introducing these factors to degenerated muscles in the urinary
 CC system can improve UI by enhancing both their integrity and neural
 CC innervation
 XX
 SQ Sequence 3600 BP; 733 A; 1099 C; 1042 G; 726 T; 0 U; 0 Other;
 Query Match 39.7%; Score 1719; DB 2; Length 3600;
 Best Local Similarity 90.8%; Pred. No. 4.3e-180;
 Matches 1923; Conservative 0; Mismatches 5; Indels 191; Gaps 1;
 Qy 2214 CCAGCTTTTGTCCCTTTAGTGAGGGTTAATTCGAGCTTTGGCGTAATCATGTGCATAGC 2273
 Db 20 CCAGCTTTTGTCCCTTTAGTGAGGGTTAATTCGAGCTTTGGCGTAATCATGTGCATAGC 79
 Qy 2274 TGTTCCTGTGTAATTTGTTATCCGCTCAAAATCCACAACATACGAGCCGGAAGCA 2333
 Db 80 TGTTCCTGTGTAATTTGTTATCCGCTCAAAATCCACAACATACGAGCCGGAAGCA 139
 Qy 2334 TAAAGTGTAAGCTGGGGTCCCTAATGAGTGAGCTAACTCACATTAATTCGCTTGGCT 2393
 Db 140 TAAAGTGTAAGCTGGGGTCCCTAATGAGTGAGCTAACTCACATTAATTCGCTTGGCT 199
 Qy 2394 CACTGCCCGCTTTCCAGTCGGGAAACCTGCTGCCAGCTGCATTAATGAATCGGCCAAC 2453
 Db 200 CACTGCCCGCTTTCCAGTCGGGAAACCTGCTGCCAGCTGCATTAATGAATCGGCCAAC 259
 Qy 2454 GCGCGGGAGAGCGGGTTTCGCTATTGGGCGCTCTTCGCTTCTCCTCACTGACTCGC 2513
 Db 260 GCGCGGGAGAGCGGGTTTCGCTATTGGGCGCTCTTCGCTTCTCCTCACTGACTCGC 319
 Qy 2514 TGGCTCGGTCGTTCCGCTCGCGCGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGGT 2573
 Db 320 TGGCTCGGTCGTTCCGCTCGCGCGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGGT 379
 Qy 2574 TATCCACAGAAATCAGGGGATAACGAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAG 2633
 Db 380 TATCCACAGAAATCAGGGGATAACGAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAG 439
 Qy 2634 CAGGACCGTAAAGGCGCGCTTCTGCTGGCTTTTCCATAGCTCCGCCCTCGAGC 2693
 Db 440 CAGGACCGTAAAGGCGCGCTTCTGCTGGCTTTTCCATAGCTCCGCCCTCGAGC 499
 Qy 2694 AGCATCAAAAATTCGACCGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGAT 2753
 Db 500 AGCATCAAAAATTCGACCGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGAT 559
 Qy 2754 ACCAGCGTTTCCCTGGAAGCTCCCTCGGCTCTCTCTGTTCCGACCTGCGGCTTA 2813
 Db 560 ACCAGCGTTTCCCTGGAAGCTCCCTCGGCTCTCTCTGTTCCGACCTGCGGCTTA 619
 Qy 2814 CCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAAGCGTGGCGCTTCTCAATGCTCAGCT 2873
 Db 620 CCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAAGCGTGGCGCTTCTCAATGCTCAGCT 679


```
Qy 2874 GTAGTATCTCAGTTCGGTGTAGTTCGTTCCCAAGCTGGCTGTGTGACGAACCCC 2933
Dy |||||
Dy 680 GTAGTATCTCAGTTCGGTGTAGTTCGTTCCCAAGCTGGCTGTGTGACGAACCCC 739
Qy 2934 CCGTTACGCCGACCGCTGCGCTTATCCGGTAACTATCGTTCGTGATCCAAACCGGTAA 2993
Dy |||||
Dy 740 CCGTTACGCCGACCGCTGCGCTTATCCGGTAACTATCGTTCGTGATCCAAACCGGTAA 799
Qy 2994 GACACGACTATCGCACTGCGCAGCAGCCACTGGTAAACAGATTAGCAGAGCGAGGTATG 3053
Dy |||||
Dy 800 GACACGACTATCGCACTGCGCAGCAGCCACTGGTAAACAGATTAGCAGAGCGAGGTATG 859
Qy 3054 TAGCGGTGCTACAGAGTCTTTGAAGTGTGGCTTAACCTACGGCTACACTAGAAGGACAG 3113
Dy |||||
Dy 860 TAGCGGTGCTACAGAGTCTTTGAAGTGTGGCTTAACCTACGGCTACACTAGAAGGACAG 919
Qy 3114 TATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAGAGTTTGGTAGCTCTT 3173
Dy |||||
Dy 920 TATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAGAGTTTGGTAGCTCTT 979
Qy 3174 GATCCGGCAAAACAAACCAACCGCTGTAGCGGTGGTTTTTTTGTGCAAGCAGCAGATT 3233
Dy |||||
Dy 980 GATCCGGCAAAACAAACCAACCGCTGTAGCGGTGGTTTTTTTGTGCAAGCAGCAGATT 1039
Qy 3234 CCGCAGAAAAAAGGATCTCAAGAGATCCTTTGATCTTTTCTACGGGTCTGACGCTC 3293
Dy |||||
Dy 1040 CCGCAGAAAAAAGGATCTCAAGAGATCCTTTGATCTTTTCTACGGGTCTGACGCTC 1097
Qy 3294 AGTGAACGAAACTCACGTTAAGGATTTTGGTCATGACGGATACATATTTGATGTA 3353
Dy |||||
Dy 1098 ----- 1097
Qy 3354 TTTAGAAAAATAACAAATAGGGGTTCCGCGCACATTTCCCGCAAAAGTGCCACCTGTAT 3413
Dy |||||
Dy 1098 ----- 1097
Qy 3414 GCGGTGTGAATATACCCACAGATGCGTAAGGAGAAAAATACCGCATCAGGAAATGTAAGC 3473
Dy |||||
Dy 1098 ----- 1097
Qy 3474 GTTAATATTCAGAGAACTCGTCAAGAGCGATAGAGCGATGCGTGGATCCGG 3533
Dy |||||
Dy 1098 -----TCAGAGAACTCGTCAAGAGCGATAGAGCGATGCGTGGATCCGG 1148
Qy 3534 AGCGCGATACCGTAAAGCACAGGAAAGCGGTACGCCATTCGCGCCAAAGCTCTTCAGC 3593
Dy |||||
Dy 1149 AGCGCGATACCGTAAAGCACAGGAAAGCGGTACGCCATTCGCGCCAAAGCTCTTCAGC 1208
Qy 3594 AATATCAGCGGTAGCCAAAGCTATGTCTGTATAGCGGTCCGCCACACCCAGCGGCCACA 3653
Dy |||||
Dy 1209 AATATCAGCGGTAGCCAAAGCTATGTCTGTATAGCGGTCCGCCACACCCAGCGGCCACA 1268
Qy 3654 GTCGATGATCCAGAAAGCGCCATTTTCCACCATGATATTCGCAAGCAGCATCGCC 3713
Dy |||||
Dy 1269 GTCGATGATCCAGAAAGCGCCATTTTCCACCATGATATTCGCAAGCAGCATCGCC 1328
Qy 3714 ATGGGTACGACGAGATCCTCGCGTGGGCGATGCTCGCTTTGAGCTCGCGCAACAGTTTC 3773
Dy |||||
Dy 1329 ATGGGTACGACGAGATCCTCGCGTGGGCGATGCTCGCTTTGAGCTCGCGCAACAGTTTC 1388
Qy 3774 GCGTGGCGGAGCCCTGATGCTCTTCGTCAGATCATCTGATCGAAGACCGGCTTC 3833
Dy |||||
Dy 1389 GCGTGGCGGAGCCCTGATGCTCTTCGTCAGATCATCTGATCGAAGACCGGCTTC 1448
Qy 3834 CATCCGATGATGCTCGCTCGATGCGATGTTTTCGCTTGGTTCGAATGGGCGAGTAGC 3893
Dy |||||
Dy 1449 CATCCGATGATGCTCGCTCGATGCGATGTTTTCGCTTGGTTCGAATGGGCGAGTAGC 1508
Qy 3894 CCGATCAAGCGTATGAGCGCGCCATTCGATCAGCCATGATGATATCTTTCGCGCAGG 3953
Dy |||||
Dy 1509 CCGATCAAGCGTATGAGCGCGCCATTCGATCAGCCATGATGATATCTTTCGCGCAGG 1568
```

```
Qy 3954 AGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACCTTGGCCCAATAGCAGCCAGTCCCT 4013
Dy |||||
Dy 1569 AGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACCTTGGCCCAATAGCAGCCAGTCCCT 1628
Qy 4014 TCCCGCTTCAGTGAACAACGTCGACACAGCTGCGCAAGGAACGCCGTCGTGGCCAGCCA 4073
Dy |||||
Dy 1629 TCCCGCTTCAGTGAACAACGTCGACACAGCTGCGCAAGGAACGCCGTCGTGGCCAGCCA 1688
Qy 4074 CGATAGCGCGCTCGCTCTTCAGTTCATTCAGGGCACCGGACAGGTGCGTCTTGAC 4133
Dy |||||
Dy 1689 CGATAGCGCGCTCGCTCTTCAGTTCATTCAGGGCACCGGACAGGTGCGTCTTGAC 1748
Qy 4134 AAAAAAGAACCGGGCGCCCTGCGCTGACAGCCGGAACACCGCGGCATCAGAGCCGAT 4193
Dy |||||
Dy 1749 AAAAAAGAACCGGGCGCCCTGCGCTGACAGCCGGAACACCGCGGCATCAGAGCCGAT 1808
Qy 4194 TGTCTGTTGTGCCAGTCATAGCCGAATAGCTCTCCACCCAGCGCGCGAGAACCTTGC 4253
Dy |||||
Dy 1809 TGTCTGTTGTGCCAGTCATAGCCGAATAGCTCTCCACCCAGCGCGCGAGAACCTTGC 1868
Qy 4254 GTCAATCCATCTTTGTTCAATCATGCGAAACGATCCTCATCTCTTGTATCAGAGCT 4313
Dy |||||
Dy 1869 GTCAATCCATCTTTGTTCAATCATGCGAAACGATCCTCATCTCTTGTATCAGAGCT 1928
Qy 4314 TGATCCCTGCGCCATCAG 4332
Dy |||||
Dy 1929 TGATCCCTGCGCCATCAG 1947

RESULT 14
AAV40795
ID AAV40795 standard; DNA; 3600 BP.
AC AAV40795;
XX
DT 23-SEP-1998 (first entry)
XX
DE Expected sequence of IGF-I containing plasmid pIG0552.
XX
KW IGF-I; insulin-like growth factor I; skeletal alpha-actin gene promoter;
KW muscle atrophy; diabetes; osteoporosis; growth disorder; therapy; AIDS;
KW Chacot-marie-tooth disease; atherogenesis; haemophilia; neuropathy; ss.
XX Synthetic.
XX
PN WO9824922-A1.
XX
PD 11-JUN-1998.
XX
PF 01-DEC-1997; 97WO-US021852.
XX
PR 02-DEC-1996; 96US-0031539P.
PR 19-NOV-1997; 97US-00974572.
XX
PA (GENE-) GENEMEDICINE INC.
PA (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI Coleman M, Schwartz R, Demayo FJ;
XX
XX WPI; 1998-333339/29.
XX
PT New vector for expression of insulin-like growth factor-I - containing a
PT skeletal alpha-actin gene promoter, IGF-I coding sequences and a 3'
PT region from growth hormone 3'-UTR.
XX
PS Claim 16; Page 37-41; 115pp; English.
XX
CC This sequence is the expected sequence for pIG0552 which is an example of
CC a vector of the invention. The vector is for expression of a nucleic acid
CC sequence in a cell, and comprises: (a) a nucleic acid cassette containing
CC a sequence encoding insulin-like growth factor-I (IGF-I); (b) a 5'
CC flanking region including one or more sequences necessary for expression
CC of the nucleic acid cassette, including a promoter from a skeletal alpha-
```

Qy	2214	CCAGCTTTTGTTCCCTTTAGTGAGGGTTAAATTTGAGAGCTTGGCGTAAATCATGTGCTATAGC	2273
Db	20	CCAGCTTTTGTTCCCTTTAGTGAGGGTTAAATTTGAGAGCTTGGCGTAAATCATGTGCTATAGC	79
Qy	2274	TGTTTTCGTGTGTAATTTGTTATCCGCTCACAATTCACACAAATACGAGCCGGAAGCA	2333
Db	80	TGTTTTCGTGTGTAATTTGTTATCCGCTCACAATTCACACAAATACGAGCCGGAAGCA	139
Qy	2334	TAAAGTGTAAAGCCTGGGGTGCCTAAATGAGTGAGCTAACTCACATTAATTCGTTTGGCT	2393
Db	140	TAAAGTGTAAAGCCTGGGGTGCCTAAATGAGTGAGCTAACTCACATTAATTCGTTTGGCT	199
Qy	2394	CAC TGCCCGCTTTCCAGTCGCGAAACCTGTCGTGCCAGTCACTCAAAAGCGGTAAATGAAATCGGCCAAC	2453
Db	200	CAC TGCCCGCTTTCCAGTCGCGAAACCTGTCGTGCCAGTCACTCAAAAGCGGCCAAC	259
Qy	2454	GCGCGGGAGAGGCGGTTTGCGTATTTGGGCGCTCTTCGGCTTCCTCGCTCACTGACTGCG	2513
Db	260	GCGCGGGAGAGGCGGTTTGCGTATTTGGGCGCTCTTCGGCTTCCTCGCTCACTGACTGCG	319
Qy	2514	TGCCTCGCTCGTTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAAGCGGTAAATGACGT	2573
Db	320	TGCCTCGCTCGTTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAAGCGGTAAATGACGT	379
Qy	2574	TATCCACAGATCAGGGATTAACGCAGGAAAGACATGTGAGCAAAAAGGCCAGCAAAAGG	2633
Db	380	TATCCACAGATCAGGGATTAACGCAGGAAAGACATGTGAGCAAAAAGGCCAGCAAAAGG	439
Qy	2634	CCAGGAACCGTAAAGAGCCGCTTGCTGGCGTTTTCATAGAGCTCGCGCCCTCGACG	2693
Db	440	CCAGGAACCGTAAAGAGCCGCTTGCTGGCGTTTTCATAGAGCTCGCGCCCTCGACG	499
Qy	2694	AGCATCAAAAAATCGACGCTCAAGTCAGAGTGGCGGCAAAACCCACAGGACTATAAAGT	2753
Db	500	AGCATCAAAAAATCGACGCTCAAGTCAGAGTGGCGGCAAAACCCACAGGACTATAAAGT	559
Qy	2754	ACCAAGGGTTTTCCCGCTGGAAGCTCCCTCGTCGCGCTCTCTGTTCGAGACCTGCGCGTTA	2813
Db	560	ACCAAGGGTTTTCCCGCTGGAAGCTCCCTCGTCGCGCTCTCTGTTCGAGACCTGCGCGTTA	619
Qy	2814	CCGATACCTGTCGCGCTTTCTCCCTTCGGGAAAGGTGGCGCTTTCTCAATGCTCAGCT	2873
Db	620	CCGATACCTGTCGCGCTTTCTCCCTTCGGGAAAGGTGGCGCTTTCTCAATGCTCAGCT	679
Qy	2874	GTAGGTATCTCAGTTTCGGTGTAGGTCGTTCCGCTCCAGCTGGGCTGTGACGAAACCC	2933
Db	680	GTAGGTATCTCAGTTTCGGTGTAGGTCGTTCCGCTCCAGCTGGGCTGTGTCAGAAACCC	739
Qy	2934	CCGTTACGCCGACCGCTGCGCCTTATCCCGGTAACTATCGTCTTTGAGTCCAAACCCGGTAA	2993

Db 1629 TCCGCTTTCAGTACAACTGAGCACAGCTGCCGAAAGAACGCCCGCTGCGCCAGCCA 1698
Qy 4074 CGATAGCCGCTGCTGCTCTGAGTTCATTTCAGGGCACGGACAGGTGCTTTCGAC 4133
Db 1699 CGATAGCCGCTGCTGCTCTGAGTTCATTTCAGGGCACGGACAGGTGCTTTCGAC 1748
Qy 4134 AAAAAGAACCGGGGCCCCCTGCTGACAGCCGGAAACAGCGGGCATCAGAGCAGCCGAT 4193
Db 1749 AAAAAGAACCGGGGCCCCCTGCTGACAGCCGGAAACAGCGGGCATCAGAGCAGCCGAT 1808
Qy 4194 TGTCTGTTGTCCTAGTATAGCCGAATAGCTCTCCACCCCAAGCGGCGGAGACCTGC 4253
Db 1809 TGTCTGTTGTCCTAGTATAGCCGAATAGCTCTCCACCCCAAGCGGCGGAGACCTGC 1868
Qy 4254 GTGCAATCCATCTGTTCAATCATCGAAACGATCCTCATCTGCTCTTTCATCAGAGCT 4313
Db 1869 GTGCAATCCATCTGTTCAATCATCGAAACGATCCTCATCTGCTCTTTCATCAGAGCT 1928
Qy 4314 TGATCCCTGCGCCATCAG 4332
Db 1929 TGATCCCTGCGCCATCAG 1947

RESULT 15
ID AAX88055 standard; DNA; 5707 BP.
AC AAX88055;
XX
DT 08-SEP-1999 (first entry)
XX
DE Plasmid pIG0335 DNA.
XX
KW Plasmid pIG0335; expression vector; treatment; disease;
KW RNA stability element; gene therapy; muscle atrophy; neurological;
KW muscular disease; systemic disease; aging; trophic factor; haemophilia;
KW clotting factor; atherosclerosis; atherosclerotic; cardiovascular;
KW cerebrovascular; peripheral-vascular disease; hormone deficiency;
KW diabetes; transgenic animal; carcinogen; regulatory element;
KW livestock improvement; immune response; ds.
XX
OS Synthetic.
XX
XX US5925564-A.
XX
XX 20-JUL-1999.
XX
XX 07-JUN-1995; 95US-00472809.
XX
XX 06-NOV-1991; 91US-00789919.
XX
XX 09-MAR-1994; 94US-00209846.
XX
XX (BAYU) BAYLOR COLLEGE MEDICINE.
XX
XX O'malley BW, Demayo FJ, Schwartz RJ;
XX
XX WPI; 1999-418276/35.
XX
XX New expression vector system useful for gene therapy.
XX
XX Disclosure; Fig 17-17P; 67pp; English.
XX
XX This invention describes novel expression vector systems containing RNA
XX stability elements from 3' flanking sequences used for establishing
XX expression of a nucleic acid sequence within a tissue. The vectors also
XX facilitate enhanced expression in tissues and target expression with
XX tissue specificity. The expression vectors can be used to treat diseases
XX through gene therapy by targeting the vector to specific tissues.
XX Diseases that can be treated include muscle atrophy associated with
XX neurological, muscular or systemic disease, aging by causing tissues to
XX express trophic factors, haemophilia by causing tissues to express and
XX secrete clotting factor into the circulation, atherosclerosis and
XX atherosclerotic cardiovascular, cerebrovascular or peripheral-vascular

CC disease by causing tissues to express factors involved in tissue
CC metabolism. They can be used to replace genes of inherited genetic
CC defects or acquired hormone deficiencies e.g. diabetes. To transform
CC cells to produce particular proteins or RNA in vitro. To create
CC transgenic animals which can be used for research into human diseases,
CC assessing novel therapeutic methods, assessing the effect of chemical and
CC physical carcinogens and for studying the effect of genes and genetic
CC regulatory elements or livestock improvement. They can be used to induce
CC an immune response. These vectors provide controlled expression of the
CC genes they carry and produce a significantly high level of expression.
CC Using 3'UTR sequences reduces the decay rates of the mRNAs encoded by the
CC vectors which causes increased expression
XX
SQ Sequence 5707 BP; 1221 A; 1634 C; 1576 G; 1276 T; 0 U; 0 Other;

Query Match 39.7%; Score 1719; DB 2; Length 5707;
Best Local Similarity 90.8%; Pred. No. 3.8e-180;
Matches 1923; Conservative 0; Mismatches 5; Indels 191; Gaps 1;

Qy 2214 CCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTCGCGTAAATCATGGTCATAGC 2273
Db 3477 CCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTCGCGTAAATCATGGTCATAGC 3536

Qy 2274 TGTTCCTGTCGAAATTTGTTATCCGCTCAAAATTCACAAACATACGAGCCGAAGCA 2333
Db 3537 TGTTCCTGTCGAAATTTGTTATCCGCTCAAAATTCACAAACATACGAGCCGAAGCA 3596

Qy 2334 TAAAGTGTAAGCCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTTGGTTGCGCT 2393
Db 3597 TAAAGTGTAAGCCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTTGGTTGCGCT 3656

Qy 2394 CACTGCCCGCTTTCAGTTCGGGAAACCTGTGTCGACGTGCATTAATGAATCGGCCAAC 2453
Db 3657 CACTGCCCGCTTTCAGTTCGGGAAACCTGTGTCGACGTGCATTAATGAATCGGCCAAC 3716

Qy 2454 GCGCGGGGAGAGCGGTTTGGCGCTATTGGCGCTCTTCGCTTCCTTCGCTCACTGACTCGC 2513
Db 3717 GCGCGGGGAGAGCGGTTTGGCGCTATTGGCGCTCTTCGCTTCCTTCGCTCACTGACTCGC 3776

Qy 2514 TCGCTCGGTTCGTTCCGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGGGTAATACGGT 2573
Db 3777 TCGCTCGGTTCGTTCCGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGGGTAATACGGT 3836

Qy 2574 TATCCACAGATCAGGGATACGAGGAAAGAAATGTGAGCAAAAGCCAGCAAAAGG 2633
Db 3837 TATCCACAGATCAGGGATACGAGGAAAGAAATGTGAGCAAAAGCCAGCAAAAGG 3896

Qy 2634 CCAGGAAACCGTAAAGGCGCGTTGCTGGCGCTTTTCCATAGGCTCGCCCCCTGACG 2693
Db 3897 CCAGGAAACCGTAAAGGCGCGTTGCTGGCGCTTTTCCATAGGCTCGCCCCCTGACG 3956

Qy 2694 AGCATCACAAAATCGACGCTCAAGTCAGAGTGGGGAAACCCGACAGGACTATAAGAT 2753
Db 3957 AGCATCACAAAATCGACGCTCAAGTCAGAGTGGGGAAACCCGACAGGACTATAAGAT 4016

Qy 2754 ACCAGGCTTTCCCTCGAAGCTCCCTCGTGGCTCTCCTGTCGAGCCCTGCGCCCTTA 2813
Db 4017 ACCAGGCTTTCCCTCGAAGCTCCCTCGTGGCTCTCCTGTCGAGCCCTGCGCCCTTA 4076

Qy 2814 CCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTACGCT 2873
Db 4077 CCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTACGCT 4136

Qy 2874 GTAGGTATCTAGTTCGGTGTAGGTGCTTCGCTCCAAAGCTGGGCTGTGTGCAGAACCCC 2933
Db 4137 GTAGGTATCTAGTTCGGTGTAGGTGCTTCGCTCCAAAGCTGGGCTGTGTGCAGAACCCC 4196

Qy 2934 CCGTTCCAGCCCGACCGCTCGGCTTATCCGTAACCTATCCTCTTGAGTCCAAACCCGGTAA 2993
Db 4197 CCGTTCCAGCCCGACCGCTCGGCTTATCCGTAACCTATCCTCTTGAGTCCAAACCCGGTAA 4256

Qy 2994 GACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTAGCAGAGCGAGGTATG 3053

Db	4257	GACACGACTTATCGCCTGCGCAGCAGCCACTGGTAAACAGATTAGCAGAGCGAGGTATG	4316	Qy	4134	AAAAAGAACCGGGCGCCCTGCGCTGACAGCCGGAACACCGCGGCATCAGAGCAGCGAT	4193
Qy	3054	TAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTTAACCTACGCTACACTAGAGGACAG	3113	Db	5206	AAAAAGAACCGGGCGCCCTGCGCTGACAGCCGGAACACCGCGGCATCAGAGCAGCGAT	5265
Db	4317	TAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTTAACCTACGCTACACTAGAGGACAG	4376	Qy	4194	TGCTGTGTGTCGCCAGTTCATAGCCGAATAGCCTCTCCACCCCAAGCGGCCGAGAACCTGC	4253
Qy	3114	TATTTGGTATCTGGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTT	3173	Db	5266	TGCTGTGTGTCGCCAGTTCATAGCCGAATAGCCTCTCCACCCCAAGCGGCCGAGAACCTGC	5325
Db	4377	TATTTGGTATCTGGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTT	4436	Qy	4254	GTGCAATCCATCTTTGTTCAATCATGCGAAACGATCCTCATCCTCTCTTGTATCAGAGCT	4313
Qy	3174	GATCGGCAAAACAAACCCCTGGTAGCGGTGGTTTTTTTTTTGTTGTAAGCAGCAGATTA	3233	Db	5326	GTGCAATCCATCTTTGTTCAATCATGCGAAACGATCCTCATCCTCTCTTGTATCAGAGCT	5385
Db	4437	GATCGGCAAAACAAACCCCTGGTAGCGGTGGTTTTTTTTTTGTTGTAAGCAGCAGATTA	4496	Qy	4314	TGATCCCTCGGCCATCAG	4332
Qy	3234	CGCGCAGAAAAAAGGATCTCAAGAGATCTTTGATCTTTTCTACGGGGTCTCAGCGTC	3293	Db	5386	TGATCCCTCGGCCATCAG	5404
Db	4497	CGCGCAGAAAAAAGGATCTCAAGAGATCTTTGATCTTTTCTACGGGGTCTCAGCGC--	4554				
Qy	3294	AGTGGAAACGAAACTCACTGTTAAGGGAATTTGGTTCATGAGCGGATACATATTTGAATGTA	3353				
Db	4555	-----	4554				
Qy	3354	TTTAGAAAAATAACAATAAGGGTTCCGCCACATTTCCCGGAAAGTGCCACCTGTAT	3413				
Db	4555	-----	4554				
Qy	3414	CGCGTGTGAANTACCGCACAGATGCGTAAAGAGAAATACCGCATCAGGAATTTGTAAGC	3473				
Db	4555	-----	4554				
Qy	3474	GTTAATAATTCAGAAGAACTCGTCAAGAAGCGATAGAAGCGGATGGCTGCGAATCGGG	3533				
Db	4555	-----TCAGAAGAACTCGTCAAGAAGCGGATAGAAGCGGATGGCTGCGAATCGGG	4605				
Qy	3534	AGCGCGGATACCGTAAAGCAGAGAGCGGTGAGCCCATTCGCCGCCAGCTTTCAGC	3593				
Db	4606	AGCGCGGATACCGTAAAGCAGAGAGCGGTGAGCCCATTCGCCGCCAGCTTTCAGC	4665				
Qy	3594	AATATCAGGGTAGCACAACGCTATGTCTGATAGCGGTCCGCCACACCCAGCGGCCACA	3653				
Db	4666	ANTATCAGGGTAGCACAACGCTATGTCTGATAGCGGTCCGCCACACCCAGCGGCCACA	4725				
Qy	3654	GTGATGAATCCAGAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCC	3713				
Db	4726	GTGATGAATCCAGAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCC	4785				
Qy	3714	ATGGGTACAGCAGAGATCTCGCGTGGGATGCTCGCCCTTGAAGCTGGCGAACAGTTC	3773				
Db	4786	ATGGGTACAGCAGAGATCTCGCGTGGGATGCTCGCCCTTGAAGCTGGCGAACAGTTC	4845				
Qy	3774	GGCTGGCGCAGCGCCCTGATGCTCTTGTCCAGATCATCTGATCGACAAGACCGGCTTC	3833				
Db	4846	GGCTGGCGCAGCGCCCTGATGCTCTTGTCCAGATCATCTGATCGACAAGACCGGCTTC	4905				
Qy	3834	CATCCGAGTACGTCTGCTCGATGCGATGTTTCGCTTGGTGGTTCGAATGGGCAGGTAGC	3893				
Db	4906	CATCCGAGTACGTCTGCTCGATGCGATGTTTCGCTTGGTGGTTCGAATGGGCAGGTAGC	4965				
Qy	3894	CGGATCAAGCGTATGCAAGCCCGCATTTGCATCAGCCATGATGGATACTTTCTCGGCAGG	3953				
Db	4966	CGGATCAAGCGTATGCAAGCCCGCATTTGCATCAGCCATGATGGATACTTTCTCGGCAGG	5025				
Qy	3954	AGCAAGGTGAGATGACAGGAGATCTTCCCGCGCATTTCCGCCCAATAGCAGCCAGTCCCT	4013				
Db	5026	AGCAAGGTGAGATGACAGGAGATCTTCCCGCGCATTTCCGCCCAATAGCAGCCAGTCCCT	5085				
Qy	4014	TCCCGCTTTCAGTGACAAGCTCGAGCAGAGTTCGCGCAAGGAACGCCGCTCGTGGCCAGCCA	4073				
Db	5086	TCCCGCTTTCAGTGACAAGCTCGAGCAGAGTTCGCGCAAGGAACGCCGCTCGTGGCCAGCCA	5145				
Qy	4074	CGATAGCGCGCTCGCTTCTGCTGCTTCAATTCAGGGCACCGGACAGGTCGGTCTTGAC	4133				
Db	5146	CGATAGCGCGCTCGCTTCTGCTGCTTCAATTCAGGGCACCGGACAGGTCGGTCTTGAC	5205				

Search completed: March 15, 2006, 20:09:34
Job time : 2325 secs

This Page Blank (uspto)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2006, 20:00:57 ; Search time 15841 Seconds
(without alignments)
12794.750 Million cell updates/sec

Title: US-10-811-028A-1

Perfect score: 4331

Sequence: 1 cggtcgggcctcttcgcta.....ttgatccctgcgcaccag 4332.

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_hc.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_ges1.*
10: gb_ges2.*
11: gb_ges3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1003.6	23.2	1186	8	DR045845 FP-10_F08
2	993.2	22.9	1176	8	CX943193 LamjGestG
3	990.6	22.9	1067	1	AU081137 AU081137
4	959.2	22.1	1089	1	AU081124 AU081124
5	898.4	20.7	1049	10	CL021189 CH216-8A1
6	896.6	20.7	1191	8	DR045882 FP-11_A09
7	896.2	20.7	925	6	CB686151 Bn01b_020
8	871	20.1	951	8	CV983341 UMC-bcf_0
9	867.8	20.0	1073	6	CF269652 FcylcolD8
10	854.4	19.7	885	10	CL076016 CH216-138
11	853.6	19.7	1195	8	DR046031 FP-8_F02
12	852	19.7	875	8	CX012952 i062d12.b
13	822.2	19.0	1163	1	AU081044 AU081044
14	821.2	19.0	868	8	CV984340 UMC-bov_0
15	819.6	18.9	1169	10	AG332951 Mus_muscu
16	818.4	18.9	1025	10	CL021193 CH216-8A1
17	813.8	18.8	833	8	CX013029 i062h07.b
18	809.8	18.7	894	8	DN641029 UMC-bend
19	806.4	18.6	935	7	CK284786 EST747508
20	805	18.6	813	8	CX006605 i023f10.b
21	804.4	18.6	966	9	EZ570738 msh2_1513
22	804.2	18.6	865	7	CK125894 BES182411

c	23	801.6	18.5	833	6	CB686421	CB686421	Bn01b_04j
c	24	795.6	18.4	804	8	CV979032	CV979032	UMC-bemiv
c	25	790.8	18.3	811	7	CK288185	CK288185	EST750307
c	26	789.8	18.2	804	7	CK291519	CK291519	EST754233
c	27	789.8	18.2	856	7	CK287297	CK287297	EST750019
c	28	789.8	18.2	910	7	CK287930	CK287930	EST750652
c	29	789.8	18.2	933	7	CK291799	CK291799	EST754513
c	30	789.8	18.2	936	7	CK256977	CK256977	EST740614
c	31	789.8	18.2	947	7	CK298208	CK298208	EST760922
c	32	789.8	18.2	954	7	CK283361	CK283361	EST746083
c	33	783.6	18.1	886	8	DN818689	DN818689	UMC-bconb
c	34	781.6	18.0	808	11	DE103081	DE103081	Oryzias 1
c	35	781.6	18.0	810	11	DE097025	DE097025	Oryzias 1
c	36	781.6	18.0	810	11	DE097277	DE097277	Oryzias 1
c	37	781.6	18.0	810	11	DE097360	DE097360	Oryzias 1
c	38	781.6	18.0	810	11	DE097448	DE097448	Oryzias 1
c	39	781.6	18.0	810	11	DE097511	DE097511	Oryzias 1
c	40	781.6	18.0	810	11	DE098632	DE098632	Oryzias 1
c	41	781.6	18.0	810	11	DE099849	DE099849	Oryzias 1
c	42	781.6	18.0	810	11	DE100113	DE100113	Oryzias 1
c	43	781.6	18.0	810	11	DE102302	DE102302	Oryzias 1
c	44	781.6	18.0	810	11	DE104910	DE104910	Oryzias 1
c	45	781.6	18.0	810	11	DE104989	DE104989	Oryzias 1

ALIGNMENTS

RESULT 1
DR045845
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
ORIGIN

DR045845 1186 bp mRNA linear EST 02-JUN-2005
FP-10_F08.SQ cDNA library of Phaeosphaeria nodorum grown on wheat cell walls Phaeosphaeria nodorum cDNA, mRNA sequence.
DR045845
DR045845.1 GI:66909681
EST.
Phaeosphaeria nodorum
Phaeosphaeria nodorum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Phaeosphaeriaceae; Phaeosphaeria.
1 (bases 1 to 1186)
Blindschneider, L.V., Cooper, R.M., Thomas, S.W., Madrid, M.P. and Oliver, R.P.
cDNA library of Phaeosphaeria nodorum grown on wheat cell walls
Unpublished (2005)
Contact: Richard Oliver
Australian Centre for Necrotrophic Fungal Pathogens (ACNFP)
Murdoch University
South Street, Murdoch, W.A 6150, Australia
Tel: +0893607404
Email: roliver@murdoch.edu.au.

Location/Qualifiers
1..1186
/organism="Phaeosphaeria nodorum"
/mol_type="mRNA"
/db_xref="taxon:13684"
/clone_lib="cDNA library of Phaeosphaeria nodorum grown on wheat Cell walls"

Query Match 23.2%; Score 1003.6; DB 8; Length 1186;
Best Local Similarity 98.9%; Pred. No. 8.3e-222;
Matches 1031; Conservative 0; Mismatches 9; Indels 2; Gaps 2;
QY 2256 CGTAATCATGCTATAGCTGTTTCTCTGTGTGAATTTATCGCTCACAAATCCACACA 2315
DB 23 CGTAATCATGCTATAGCTGTTTCTCTGTGTGAATTTATCGCTCACAAATCCACACA 82
QY 2316 ACATAGAGCCGGAAGCAATAAGTGTAAAGCCCTGGGGTGCCTAATGAGTGAGCTCACTCA 2375
DB 83 ACATAGAGCCGGAAGCAATAAGTGTAAAGCCCTGGGGTGCCTAATGAGTGAGCTCACTCA 142
QY 2376 CATTAATTCGTTGCGCTCACTCGCCGCTTTTCAGTCGGGGAACCTGTCGTCGACGTCG 2435


```
Db      143  CATTAAATGGCTTCGCTCACTGCCCGCTTTCAGTCCGGAACCTGCTCGTCCAGCTGC 202
      |||
Qy      2436  ATTAATGAATCGGCAAGCGCGGGAGAGCGGTTTGGCTATTGGGCGCTCTCCGCTT 2495
      |||
Db      203  ATTAATGAATCGGCCAAACGCGCGGGAGAGCGGTTTGGCTATTGGGCGCTCTCCGCTT 262
      |||
Qy      2496  CCTCGCTCACTGACTCGCTGGCTCGGTTCGCTTCGGCTGCGGCGAGCGGTATCAGCTCACT 2555
      |||
Db      263  CCTCGCTCACTGACTCGCTGGCTCGGTTCGCTTCGGCTGCGGCGAGCGGTATCAGCTCACT 322
      |||
Qy      2556  CAAAGGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACGCGAGGAAGAAATGTGAG 2615
      |||
Db      323  CAAAGGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACGCGAGGAAGAAATGTGAG 382
      |||
Qy      2616  CAAAGGCCAGCAAAAGGCCAGGAAACGTTAAAGAGCGCGCTTCGTCGCTTTTCCATA 2675
      |||
Db      383  CAAAGGCCAGCAAAAGGCCAGGAAACGTTAAAGAGCGCGCTTCGTCGCTTTTCCATA 442
      |||
Qy      2676  GGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGTGGCGAACC 2735
      |||
Db      443  GGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGTGGCGAACC 502
      |||
Qy      2736  CGACAGGACTATAAGATAACAGGCGTTTCCCTCGTGAAGCTCCCTCGTGGCTCTCCTG 2795
      |||
Db      503  CGACAGGACTATAAGATAACAGGCGTTTCCCTCGTGAAGCTCCCTCGTGGCTCTCCTG 562
      |||
Qy      2796  TTCCGACCTCGCGTTACCGGATACGTCCGCTTTCTCCCTTCGGGAAGCGTGGCG 2855
      |||
Db      563  TTCCGACCTCGCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCG 622
      |||
Qy      2856  TTTCTCAATGTCTACGCTGTAGGTATCTCAGTTCCGTTAGGTCTGCTCCGCTCCAGCTGG 2915
      |||
Db      623  TTTCTCATAGTCTACGCTGTAGGTATCTCAGTTCCGTTAGGTCTGCTCCGCTCCAGCTGG 682
      |||
Qy      2916  GCTGTGTGACGAACCCCGTTACGCCGACCGCTGCCCTTATCCGGTAACTATCGTC 2975
      |||
Db      683  GCTGTGTGACGAACCCCGTTACGCCGACCGCTGCCCTTATCCGGTAACTATCGTC 742
      |||
Qy      2976  TTGAGTCCAAACCCGTTAGACAGCACTTATGCCACTGGCAGCCACTGGTAAACAGA 3035
      |||
Db      743  TTGAGTCCAAACCCGTTAGACAGCACTTATGCCACTGGCAGCCACTGGTAAACAGA 802
      |||
Qy      3036  TTAGCAGAGCGAGGTATGTAGCGGTGTCTACAGATTCTTGAAGTGGTGGCTAACTAG 3095
      |||
Db      803  TTAGCAGAGCGAGGTATGTAGCGGTGTCTACAGATTCTTGAAGTGGTGGCTAACTAG 862
      |||
Qy      3096  GCTACACTAGAAGGACAGTATTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGA 3155
      |||
Db      863  GCTACACTAGAAGAACAGTATTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGA 922
      |||
Qy      3156  AAAGAGTTGGTAGCTCTTGATCCGCAAAACCAACCAACCGCTGGTAGCGGTGTTTTTGG 3215
      |||
Db      923  AAAGAGTTGGTAGCTCTTGATCCGCAAAACCAACCAACCGCTGGTAGCGGTGTTTTTGG 982
      |||
Qy      3216  TTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAATCTTTGATCTTTT 3275
      |||
Db      983  TTTGCAAGCAGCAGATAACGCGCAGAAAAAATGATCTCAAGAAATCTTTGATCTTTT 1040
      |||
Qy      3276  CTACGGGTTCTACGCTCAGTG 3297
      |||
Db      1041  TCTACGGGTCTACGCTCAGTG 1062
      |||
```

```
RESULT 2
CX943193
LOCUS
DEFINITION
  LamJGestGS8 Laminaria japonica Lambda Zap Express Library Laminaria
  japonica cDNA 5', mRNA sequence.
ACCESSION
  CX943193
KEYWORDS
  EST;
SOURCE
  Laminaria japonica
```

```
ORGANISM
  Laminaria japonica
  Eukaryota; stramenopiles; Phaeophyceae; Laminariales;
  Laminariaceae; Laminaria.
REFERENCE
  1 (bases 1 to 1176)
  Xuan,J., Zhao,G., Wang,W., Duan,D., Weng,M. and Wang,B.
  Expressed sequence tag analysis of the brown alga Laminaria
  japonica (Phaeophyceae)
  JOURNAL
  Unpublished (2005)
  COMMENT
  Contact: Xuan JS
  The State Key Laboratory of Plant Genome Research
  Institute of Genetics and Developmental Biology, Chinese Academy of
  Science
  Datum Road, Chaoyang District, Beijing, China, 100101
  Tel: 086 010 64889353
  Fax: 086 010 64873428
  Email: bnuxuan@hotmail.com
  Seq primer: T3 Forward
  High quality sequence stop: 1176.
```

FEATURES

```
Location/Qualifiers
  source
    1..1176
    /organism="Laminaria japonica"
    /mol_type="mRNA"
    /db_xref="taxon:88149"
    /sex="female"
    /dev_stage="gametophyte"
    /clone_lib="Laminaria japonica Lambda Zap Express Library"
    /note="Vector: Uni-ZAP@ XR vector; Site_1: EcoRI; Site_2:
    XhoI"
```

ORIGIN

```
Query Match      22.9%; Score 993.2; DB 8; Length 1176;
Best Local Similarity 97.6%; Pred. No. 2.2e-219; Indels 8; Gaps 5;
Matches 1062; Conservative 0; Mismatches 18;

Qy      2256  CGTAATCATGTCTAGCTGTTTCTGTGCAAAATTGTTATCCGCTCAAAATTCACACA 2315
      |||
Db      37   CGTAATCATGTCTAGCTGTTTCTGTGCAAAATTGTTATCCGCTCAAAATTCACACA 96
      |||
Qy      2316  ACATACGAGCGGAGCATAAAGTGTAAAGCTGGGGTGCCTATAGTAGTAACTCA 2375
      |||
Db      97   ACATACGAGCGGAGCATAAAGTGTAAAGCTGGGGTGCCTATAGTAGTAACTCA 156
      |||
Qy      2376  CATTAAATTCGCTTCGCTCACTGCCGCTTTCAGTCCGGAAACCTGTCGTCAGCTGC 2435
      |||
Db      157  CATTAAATTCGCTTCGCTCACTGCCGCTTTCAGTCCGGAAACCTGTCGTCAGCTGC 216
      |||
Qy      2436  ATTAATGAATCGGCCAACGCGCGGAGAGCGGTTTCGTAATTCGGCGCTTCCGCTT 2495
      |||
Db      217  ATTAATGAATCGGCCAACGCGCGGAGAGCGGTTTCGTAATTCGGCGCTTCCGCTT 276
      |||
Qy      2496  CCTCGCTCACTGACTCGCTCGCTCGCTTCGCTTCGGCTGGGCGAGCGGTATCAGCTCACT 2555
      |||
Db      277  CCTCGCTCACTGACTCGCTCGCTCGCTTCGCTTCGGCTGGGCGAGCGGTATCAGCTCACT 336
      |||
Qy      2556  CAAAGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACGCGAGGAAGAAATGTGAG 2615
      |||
Db      337  CAAAGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACGCGAGGAAGAAATGTGAG 396
      |||
Qy      2616  CAAAGGGCCAGCAAAAGGCCAGGAAACCGTAAAGAGCGCGGTTGCTGGGTTTTCATA 2675
      |||
Db      397  CAAAGGGCCAGCAAAAGGCCAGGAAACCGTAAAGAGCGCGGTTGCTGGGTTTTCATA 456
      |||
Qy      2676  GGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGTGGCGAACC 2735
      |||
Db      457  GGCTCCGCCCCCTGACGAGCATCACAAAATTCGACGCTCAAGTCAGAGTGGCGAACC 516
      |||
Qy      2736  CGACAGGACTATAAAGATACACAGGCGTTTCCCGCTGGAAAGCTCCCTCGTCCGCTCTCTG 2795
      |||
Db      517  CGACAGGACTATAAAGATACACAGGCGTTTCCCGCTGGAAAGCTCCCTCGTCCGCTCTCTG 576
      |||
Qy      2796  TTTCCGACCTCGCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCG 2855
      |||
Db      577  TTTCCGACCTCGCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCG 636
      |||
```

2856 TTTCTCAATGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGTTCGTTCCGCTCAAGCTGG 2915
|
|
|
637 TTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGTTCGTTCCGCTCAAGCTGG 696
|
|
|
2916 GCTGTGTGACGAAACCCCGCTTTCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTC 2975
|
|
|
697 GCTGTGTGACGAAACCCCGCTTTCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTC 756
|
|
|
2976 TTGAGTCCAAACCCCGTAAAGACACACACTTATCGCACTGGCAGCAGCCACTGGTAAACAGGA 3035
|
|
|
757 TTGAGTCCAAACCCCGTAAAGACACACACTTATCGCACTGGCAGCAGCCACTGGTAAACAGGA 816
|
|
|
3036 TTACGAGCGAGGTATGTAGCGGTGCTACAGAGTTCCTTGAAGTGTGGCTAACTACG 3095
|
|
|
817 TTACGAGCGAGGTATGTAGCGGTGCTACAGAGTTCCTTGAAGTGTGGCTAACTACG 876
|
|
|
3096 GCTACACTAGAGCAGCATTTGGTATCTGCGCTGCTGCTGAAGCCAGTTACCTTCGAA 3155
|
|
|
877 GCTACACTAGAGCAGCATTTGGTATCTGCGCTGCTGCTGAAGCCAGTTACCTTCGAA 936
|
|
|
3156 AAAGAGTTGGTAGTCTTTGATCCCGCAACAAACACCGCTGGTAGCGGTGTTTTTTG 3215
|
|
|
937 AAAGAGTTGGTAGTCTTTGATCCCGCAACAAACACCGCTGGTAGCGGTGTTTTTTG 995
|
|
|
3216 TTTCCAAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAAGATCTTTTGATCTTTT 3275
|
|
|
996 TTTCCAAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAAGATCTTTTGATCTTTT 1053
|
|
|
3276 CTACGGGGTGTAGCTCAGTGGAAAGAAACTCAGTTAAGGATTTTGTGTATGAGCG 3335
|
|
|
1054 CTAC-GGGTCTGACGCTCAGTG---ACGAAACTCAGCTT-AGGGATTTTGTGTATGAGAT 1108
|
|
|
3336 GATACATA 3343
|
|
|
1109 TATCAAAA 1116
|
|
|

RESULT 3
LOCUS AU081137
DEFINITION AU081137 Oncorhynchus mykiss Kidney infected by infectious hematopoietic necrosis virus
ACCESSION AU081137
VERSION AU081137.1 GI:6431485
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE 1 (bases 1 to 1067)
AUTHORS Kono,T., Sakai,M. and LaPatra,S.E.
TITLE Expressed Sequence Tag Analysis of Kidney and Gill Tissues from Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious Hematopoietic Necrosis Virus
JOURNAL Mar. Biotechnol. 2 (5), 493-498 (2001)
COMMENT Contact: Masahiro Sakai
Faculty of Agriculture
Miyazaki University
1-1 nishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192, Japan
Email: m.sakai@cc.miyazaki-u.ac.jp.
Location/Qualifiers
FEATURES
source 1..1067
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="K12"
/tissue_type="kidney"
/clone_lib="Oncorhynchus mykiss Kidney infected by infectious hematopoietic necrosis virus"
/note="common name:rainbow trout ; infected by infectious

hematopoietic necrosis virus"

ORIGIN
Query Match 22.9%; Score 990.6; DB 1; Length 1067;
Best Local Similarity 98.9%; Pred. No. 8.6e-219;
Matches 1018; Conservative 0; Mismatches 9; Indels 2; Gaps 2;
Qy 2210 AGCTCCAGCTTTTGTGTTCCCTTTAGTGAGGGTTAAATTTTCGAGCTTGGCGTAACTATGTGTC 2269
|
|
|
Db 41 AGCTCCAGCTTTTGTGTTCCCTTTAGTGAGGGTTAAATTTTCGAGCTTGGCGTAACTATGTGTC 100
|
|
|
Qy 2270 TAGCTGTTTCTGTGTGAAATTTGTTATCCGCTCACAATTCACACAACATACGAGCCGGA 2329
|
|
|
Db 101 TAGCTGTTTCTGTGTGAAATTTGTTATCCGCTCACAATTCACACAACATACGAGCCGGA 160
|
|
|
Qy 2330 AGCATAAAGTGTAAAGCTGGGCTGCTAATAGTGAGTGAAGTAACTCACAATTAATTTGCGTTG 2389
|
|
|
Db 161 AGCATAAAGTGTAAAGCTGGGCTGCTAATAGTGAGTGAAGTAACTCACAATTAATTTGCGTTG 220
|
|
|
Qy 2390 CGCTCACTGCCCGCTTTTCAGTCGGGAAACCTGTCGTCGCCAGCTGCAATTAATGAATCGGC 2449
|
|
|
Db 221 CGCTCACTGCCCGCTTTTCAGTCGGGAAACCTGTCGTCGCCAGCTGCAATTAATGAATCGGC 280
|
|
|
Qy 2450 CAACGCGCGGGAGAGCGGTTTTCGTTATTTGGCGCTCTTCCGCTTCTCGCTCAGTAC 2509
|
|
|
Db 281 CAACGCGCGGGAGAGCGGTTTTCGTTATTTGGCGCTCTTCCGCTTCTCGCTCAGTAC 340
|
|
|
Qy 2510 TCCTCGCTCGCTCGCTCGCTCGCGAGCGGTATCAGCTCACTCAAAAGCGGTAAATA 2569
|
|
|
Db 341 TCCTCGCTCGCTCGCTCGCTCGCGAGCGGTATCAGCTCACTCAAAAGCGGTAAATA 400
|
|
|
Qy 2570 CGGTTATCCACAGAAATCAGGGGATAACGAGGAAAGAAACATGTGAGCAAAAGGCGCAGCAA 2629
|
|
|
Db 401 CGGTTATCCACAGAAATCAGGGGATAACGAGGAAAGAAACATGTGAGCAAAAGGCGCAGCAA 460
|
|
|
Qy 2630 AAGCCGAGAACCGTAAAGAGCGGTTTCTCGCGGTTTTTTCATAGGCTCCGCGCCCT 2689
|
|
|
Db 461 AAGCCGAGAACCGTAAAGAGCGGTTTCTCGCGGTTTTTTCATAGGCTCCGCGCCCT 520
|
|
|
Qy 2690 GAGCAGCATCACAAAAATCGACCTCAAGTCAGAGTGGCGAAACCGCAGAGCACTATAA 2749
|
|
|
Db 521 GAGCAGCATCACAAAAATCGACCTCAAGTCAGAGTGGCGAAACCGCAGAGCACTATAA 580
|
|
|
Qy 2750 AGATACAGGCGTTTCCCTCGTGAAGCTCCCTCGTGGCTCTCTGTTCCGACCCCTCGCG 2809
|
|
|
Db 581 AGATACAGGCGTTTCCCTCGTGAAGCTCCCTCGTGGCTCTCTGTTCCGACCCCTCGCG 640
|
|
|
Qy 2810 CTTACCGGATACCTGTCCGCTTTTCTCCCTTCGGGAAGCGTGGGCTTTCTCAATGTCTCA 2859
|
|
|
Db 641 CTTACCGGATACCTGTCCGCTTTTCTCCCTTCGGGAAGCGTGGGCTTTCTCAATGTCTCA 700
|
|
|
Qy 2870 CGCTGTAGGTATCTCAGTTTCGGTGTAGTTCGTTTCGCTCAAGCTGGGCTGTGTGACGAA 2929
|
|
|
Db 701 CGCTGTAGGTATCTCAGTTTCGGTGTAGTTCGTTTCGCTCAAGCTGGGCTGTGTGACGAA 760
|
|
|
Qy 2930 CCCCCTGTTTCAGCCCGCAGCCGCTGCTGCTTATCCGGTAACTATCGTTGAGTCCAAACCCG 2989
|
|
|
Db 761 CCCCCTGTTTCAGCCCGCAGCCGCTGCTGCTTATCCGGTAACTATCGTTGAGTCCAAACCCG 820
|
|
|
Qy 2990 GTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTACGAGCCGAGG 3049
|
|
|
Db 821 GTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTACGAGCCGAGG 880
|
|
|
Qy 3050 TATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTTAACCTACGCTACACTAGAGG 3109
|
|
|
Db 881 TATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTTAACCTACGCTACACTAGAGG 940
|
|
|
Qy 3110 ACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTTACCTTCGGAAGAAAGAGTTGGTAGC 3169
|
|
|
Db 941 ACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTTACCTTCGGAAGAAAGAGTTGGTAGC 1000
|
|
|
Qy 3170 TCTTGATCCGGGAAACAAACCCAGCTGGTAGGCTGTTTTTTTGTTCGAGCAGCAG 3229
|
|
|

```

Db 1001 TCTTGATCCGGCAACAAA-CAACGCTGGTAGCGTGTGTTTTTTTGTGTC-AGCAGCAG 1058
Qy 3230 ATTACGCGC 3238
Db 1059 ATTACGCGC 1067

RESULT 4
AU081124 1089 bp mRNA linear EST 30-JUL-2002
LOCUS AU081124 Oncorhynchus mykiss Kidney infected by infectious
DEFINITION hematopoietic necrosis virus Oncorhynchus mykiss cDNA clone KG'12,
mRNA sequence.
ACCESSION AU081124
VERSION AU081124.1 GI:6431472
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE 1 (bases 1 to 1089)
AUTHORS Kono,T., Sakai,M. and LaPatra,S.E.
TITLE Expressed Sequence Tag Analysis of Kidney and Gill Tissues from
Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious
Hematopoietic Necrosis Virus
JOURNAL Mar. Biotechnol. 2 (5), 493-498 (2001)
COMMENT Contact: Masahiro Sakai
Faculty of Agriculture
Miyazaki University
1-1 nishi gakuenibanaadai, Miyazaki, Miyazaki 889-2192, Japan
Email: m.sakai@cc.miyazaki-u.ac.jp.
Location/Qualifiers
1..1089
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="KG'12"
/tissue_type="kidney"
/clone_lib="Oncorhynchus mykiss Kidney infected by
infectious hematopoietic necrosis virus"
/note="common name:rainbow trout ; infected by infectious
hematopoietic necrosis virus"

ORIGIN
Query Match 22.1%; Score 959.2; DB 1; Length 1089;
Best Local Similarity 97.2%; Pred. No. 1.7e-211;
Matches 1019; Conservative 0; Mismatches 23; Indels 6; Gaps 4;

Qy 2210 AGCTCAGCTTTTGTCCCTTTAGTGAGGGTTAAATTCGAGCTTGGCGTAATCATGGTCA 2269
Db 42 AGCTCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTGGCGTAATCATGGTCA 101
Qy 2270 TAGCTGTTTCCTGTGGAATTTGTTATCCGCTCACAATTCACAAACATACAGCCGGA 2329
Db 102 TAGCTGTTTCCTGTGGAATTTGTTATCCGCTCACAATTCACAAACATACAGCCGGA 161
Qy 2330 AGCATAAAGTGTAAGAGCTTGGGGTGCTTAATGAGTGAGCTAACTCACATTAATTCGGTTG 2389
Db 162 AGCATAAAGTGTAAGAGCTTGGGGTGCTTAATGAGTGAGCTAACTCACATTAATTCGGTTG 221
Qy 2390 CGCTCACTCGCGCTTTCAGTCGCGGAAACCTGTGTCGAGCTGCAATTAATGAATCGGC 2449
Db 222 CGCTCACTCGCGCTTTCAGTCGCGGAAACCTGTGTCGAGCTGCAATTAATGAATCGGC 281
Qy 2450 CAACGCGGGGAGAGCGGTTTGGCTATTGGCGCTCTCCGCTTCCTCGCTCACTGAC 2509
Db 282 CAACGCGGGGAGAGCGGTTTGGCTATTGGCGCTCTCCGCTTCCTCGCTCACTGAC 341
Qy 2510 TCGCTCGCTCGGTCTGCTCGGCTCGCGGAGCGGTATCAGCTCACTCAAAGCGGTAATA 2569
Db 342 TCGCTCGCTCGGTCTGCTCGGCTCGCGGAGCGGTATCAGCTCACTCAAAGCGGTAATA 401

```

```

Qy 2570 CGGTTATCCAGCAATCAGGGGATAACGCGAGGAAGAACATGTGAGCAAAAGGCCAGCAA 2629
Db 402 CGGTTATCCAGCAATCAGGGGATAACGCGAGGAAGAACATGTGAGCAAAAGGCCAGCAA 461
Qy 2630 AAGGCCAGGAACCGTAAAAAGGCCCGCTTGCTGCGGTTTTTTTCCATAGGCTCCGCCCCCT 2689
Db 462 AAGGCCAGGAACCGTAAAAAGGCCCGCTTGCTGCGGTTTTTTTCCATAGGCTCCGCCCCCT 521
Qy 2690 GACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAA 2749
Db 522 GACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAA 581
Qy 2750 AGATACCAAGCGTTTCCCGCTGGAAGCTCCCTGTCGGCTCTCTGTTCCGACCTCGCG 2809
Db 582 AGATACCAAGCGTTTCCCGCTGGAAGCTCCCTGTCGGCTCTCTGTTCCGACCTCGCG 641
Qy 2810 CTTACCGGATACCTGTCCGCCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGTCTA 2869
Db 642 CTTACCGGATACCTGTCCGCCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGTCTA 701
Qy 2870 CGCTGAGGTATCTCAGTTCGGTGTAGTCTGTTCCGTCCTCAAGCTGGGCTGTGTGACGAA 2929
Db 702 CGCTGAGGTATCTCAGTTCGGTGTAGTCTGTTCCGTCCTCAAGCTGGGCTGTGTGACGAA 761
Qy 2930 CCCCCGTTTCAGCCGACCGCTGCGCCTTATCCGCTAACTATCGTCTTGTAGTCCAAACCG 2989
Db 762 CCCCCGTTTCAGCCGACCGCTGCGCCTTATCCGCTAACTATCGTCTTGTAGTCCAAACCG 821
Qy 2990 GTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTTAGCAGAGCGAGG 3049
Db 822 GTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTTAGCAGAGCGAGG 881
Qy 3050 TATGTAGCGGTGTCTACAGTTCCTGAAG-TGGTGGCTAACTACGCTACACTAGAG 3108
Db 882 TATGTAGCGGTGTCTACAGTTCCTGAAGTTTGTGGCTAACTACGCTACACTAGAG 941
Qy 3109 GACAGTATTTGGTATCTGCGCTCTGCTGAACGAGTTACCTTCGGAAGAGTTGGTAG 3168
Db 942 AACAGTATTTGGTATCTGCGCTCTGCTGGAGCCAGTTACCTTCGGAAGAGTTGGTAG 1001
Qy 3169 CTCCTT-GATCGCGCAACAAACCA---CCGCTGGTAGCGTGGTGTGTTTGTGCAAGC 3224
Db 1002 CTCCTGGATCGGCAACAAACCAACCGCTGGGAAGGGGGTGTCTTTTGTGCAAGC 1061
Qy 3225 A-GCAGATTACGCGCAGAAAAAAGGAT 3251
Db 1062 ACGCAGATTACCGCGCAAAAAAACGAT 1089

RESULT 5
CL021189 1049 bp DNA linear GSS 31-DEC-2003
LOCUS CH216-8A14 RM1.1 CH216 Xenopus tropicalis genomic clone CH216-8A14,
DEFINITION genomic survey sequence.
ACCESSION CL021189
VERSION CL021189.1 GI:40463002
KEYWORDS GSS.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 1049)
AUTHORS Krenitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
Mardis,E. and Wilson,R.
TITLE A physical map of the xenopus tropicalis genome
JOURNAL Unpublished (2003)
COMMENT Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: RM1 TAGCACTCACTATAGGAGA

```

Class: BAC ends
High quality sequence start: 43
High quality sequence stop: 888.

FEATURES

Location/Qualifiers
1..1049
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-8A14"
/sex="male"
/cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis BAC library"

ORIGIN

Query Match 20.7%; Score 898.4; DB 10; Length 1049;
Best Local Similarity 98.1%; Pred. No. 2.3e-197;
Matches 930; Conservative 0; Mismatches 16; Indels 2; Gaps 2;

QY 2245 TTCGAGCTTGGCGTAATCATGTCATAGCTGTTTCTCTGTGTGAATTTGTTATCCGCTCAC 2304
DB |||||
QY 101 TGCAGCTTGGCGTAATCATGTCATAGCTGTTTCTCTGTGTGAATTTGTTATCCGCTCAC 160
DB |||||
QY 2305 AATTCCACACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGT 2364
DB |||||
QY 161 AATTCCACACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGT 220
QY 2365 GAGTAACTCATTAATTTGGTTCGCTCACTCCCGCTTCAGTCGGGAACCTGTC 2424
DB |||||
QY 221 GAGTAACTCATTAATTTGGTTCGCTCACTCCCGCTTCAGTCGGGAACCTGTC 280
QY 2425 GTGCAGCTGCTAATTAATGAAATCGCCCAACGCGCGGAGAGCGGTTTGGTATTGGCGG 2484
DB |||||
QY 281 GTGCAGCTGCTAATTAATGAAATCGCCCAACGCGCGGAGAGCGGTTTGGTATTGGCGG 340
QY 2485 CTCCTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGCTGCTGCGTTCGGTTCGGCGAGCGGT 2544
DB |||||
QY 341 CTCCTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGCTGCTGCGTTCGGTTCGGCGAGCGGT 400
QY 2545 ATCAGCTCACTCAAGCGGTGTAATACGGTTATTCACAGATCAGGAGATACGAGGAAA 2604
DB |||||
QY 401 ATCAGCTCACTCAAGCGGTGTAATACGGTTATTCACAGATCAGGAGATACGAGGAAA 460
QY 2605 GAACATGTGAGCAAAAGCCAGCAAAAGCCAGCAACCGTAAAGAGCCGCTTGGTGGC 2664
DB |||||
QY 461 GAACATGTGAGCAAAAGCCAGCAAAAGCCAGCAACCGTAAAGAGCCGCTTGGTGGC 520
QY 2665 GTTTTTCATAGGCTCCGCCCTCTGACGAGCATCACAAAATTCAGCTCAAGTCAAG 2724
DB |||||
QY 521 GTTTTTCATAGGCTCCGCCCTCTGACGAGCATCACAAAATTCAGCTCAAGTCAAG 580
QY 2725 GTGCGGAACCCGACAGACTATAAGATACAGGCGTTTCCCTCGGAAGCTCCCTCGT 2784
DB |||||
QY 581 GTGCGGAACCCGACAGACTATAAGATACAGGCGTTTCCCTCGGAAGCTCCCTCGT 640
QY 2785 GCGCTCTCTCTGTTCCGACCTTCCGCTTACCGGATACCTGTCGCCCTTCTCCCTCCGG 2844
DB |||||
QY 641 GCGCTCTCTCTGTTCCGACCTTCCGCTTACCGGATACCTGTCGCCCTTCTCCCTCCGG 700
QY 2845 AAGCGTGGCGTTTCTCAATGCTCACTGCTGAGTATCTCAGTTTCGCTGAGTTCGTTG 2904
DB |||||
QY 701 AAGCGTGGCGTTTCTCATAGCTCACTGCTGAGTATCTCAGTTTCGCTGAGTTCGTTG 760
QY 2905 CTCCAAGCTGGGCTGTGACAGAACCCCGCTTCAGCCGACCGCTGCGCTTATCCGG 2964
DB |||||
QY 761 CTCCAAGCTGGGCTGTGACAGAACCCCGCTTCAGCCGACCGCTGCGCTTATCCGG 820
QY 2965 TAACTATCGCTTGGCTGCTAAGACAGCACTTATCGCACTGGCAGCAGCCAC 3024
DB |||||
QY 821 TAACTATCGCTTGGCTGCTAAGACAGCACTTATCGCACTGGCAGCAGCCAC 880

QY 3025 TGGTAACAGGATTAGCAGAGCGAGGATGTAGCGGTGTCTACAGAGTCTTCTGAAGTGGT 3084
DB |||||
QY 881 TGGTAACAGGATTAGCAGAGCGAGGATGTAGCGGTGTCTACAGAGTCTTCTGAAGTGGT 940
DB |||||
QY 3085 GCCTAACTAGGCTACACTAGAGGAC-AGTATTGGTATCTGGCTCTGCTGAAGCCAG 3143
DB |||||
QY 941 GCCTAACTAGGCTACACTAGAGGAC-AGTATTGGTATCTGGCTCTGCTGAAGCCAG 1000
DB |||||
QY 3144 TTACC-TTCGGAAGAGTGTGTAGCTCTTGTATCGGCAACAAACC 3190
DB |||||
QY 1001 TTACCTTTCGGAAGAGTGTGTAGCTCTTGTATCGGCAAAAMAC 1048
DB |||||

RESULT 6
DR045882 1191 bp mRNA linear EST 02-JUN-2005
LOCUS FP-11_A09-SEQ cDNA library of Phaeosphaeria nodorum grown on wheat cell walls Phaeosphaeria nodorum cDNA, mRNA sequence.
DEFINITION DR045882
ACCESSION DR045882
VERSION DR045882.1 GI:66909718
KEYWORDS EST.
SOURCE Phaeosphaeria nodorum
ORGANISM Phaeosphaeria nodorum
REFERENCE 1 (bases 1 to 1191)
AUTHORS Pleosporales; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes; Bindschedler, L.V., Cooper, R.M., Thomas, S.W., Madrid, M.P. and Oliver, R.P.
TITLE cDNA library of Phaeosphaeria nodorum grown on wheat cell walls
JOURNAL Unpublished (2005)
COMMENT Contact: Richard Oliver
Australian Centre for Necrotrophic Fungal Pathogens (ACNFP)
Murdoch University
South Street, Murdoch, W.A 6150, Australia
Tel: +0893607404
Email: roliver@murdoch.edu.au.

FEATURES
source 1..1191
/organism="Phaeosphaeria nodorum"
/mol_type="mRNA"
/db_xref="taxon:13684"
/clone_lib="cDNA library of Phaeosphaeria nodorum grown on wheat cell walls"

ORIGIN
Query Match 20.7%; Score 896.6; DB 8; Length 1191;
Best Local Similarity 99.1%; Pred. No. 6e-197;
Matches 923; Conservative 0; Mismatches 4; Indels 4; Gaps 2;

QY 2210 AGCTCCAGCTTTTGTTCCTTTTAGTGAGGGTTAATTTTCGAGCTTTGGCGTAAATCATGTCA 2269
DB |||||
QY 109 AGCTCCAGCTTTTGTTCCTTTTAGTGAGGGTTAATTTTCGAGCTTTGGCGTAAATCATGTCA 168
DB |||||
QY 2270 TAGCTGTTTCTGTGTGAAATTTGTATTCGCTCACAAATTCACAAACATACAGCCGGA 2329
DB |||||
QY 169 TAGCTGTTTCTGTGTGAAATTTGTATTCGCTCACAAATTCACAAACATACAGCCGGA 228
DB |||||
QY 2330 AGCATAAAGTGTAAAGCTGGGGTGCCTAATGAGTGAGCTAACTCAATTAATTCGCTG 2389
DB |||||
QY 229 AGCATAAAGTGTAAAGCTGGGGTGCCTAATGAGTGAGCTAACTCAATTAATTCGCTG 288
DB |||||
QY 2390 CGCTCACTGCGCGCTTTTCCAGTTCGGGAAACCTGTCTGCGAGCTGCAATTAATGAATCGGC 2449
DB |||||
QY 289 CGCTCACTGCGCGCTTTTCCAGTTCGGGAAACCTGTCTGCGAGCTGCAATTAATGAATCGGC 348
DB |||||
QY 2450 CAACGCGCGGGAGAGCGGTTTTCGCTATTTGGCGCTCTTCCGCTTCTCGCTCACTGAC 2509
DB |||||
QY 349 CAACGCGCGGGAGAGCGGTTTTCGCTATTTGGCGCTCTTCCGCTTCTCGCTCACTGAC 408
DB |||||
QY 2510 TCCGCTCGCTCGGTCGTTTCGCTTCGGCTCGCGGAGCGGTATCAGCTCACTCAAAAGCGGTAA 2569
DB |||||
QY 409 TCCGCTCGCTCGGTCGTTTCGCTTCGGCTCGCGGAGCGGTATCAGCTCACTCAAAAGCGGTAA 468
DB |||||

Qy	2570	CGGTTATCCACAGAAATCAGGGGATAACGACGAAAGAAACATGTGAGCAAAAGGCCACGAA	2629
Db	469	CGGTTATCCACAGAAATCAGGGGATAACGACGAAAGAAACATGTGAGCAAAAGGCCACGAA	528
Qy	2630	AAGGCCAGGAACCGTAAAGAGCCGCGTGTGCGGTTTTCATAGGCTCCGCCCCCT	2689
Db	529	AAGGCCAGGAACCGTAAAGAGCCGCGTGTGCGGTTTTCATAGGCTCCGCCCCCT	588
Qy	2690	GACGAGATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAA	2749
Db	589	GACGAGATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAA	648
Qy	2750	AGATACACAGGCGTTTCCCTCGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCTGCGG	2809
Db	649	AGATACACAGGCGTTTCCCTCGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCTGCGG	708
Qy	2810	CTTACCGGATACCTGTCCGCTTTCTCCCTCGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCTGCTCA	2869
Db	709	CTTACCGGATACCTGTCCGCTTTCTCCCTCGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCTGCTCA	768
Qy	2870	CGCTGTAGTATCTCAGTTCGCTGTAGTGTCTGCTCCAAAGCTGGGCTGTGTGCACGAA	2929
Db	769	CGCTGTAGTATCTCAGTTCGCTGTAGTGTCTGCTCCAAAGCTGGGCTGTGTGCACGAA	828
Qy	2930	CCCCCGTTAGCCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTTGAGTCCAAACCCG	2989
Db	829	CCCCCGTTAGCCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTTGAGTCCAAACCCG	888
Qy	2990	GTAACACAGACTTATCCGCTACGACGACCTGCTGTAACGAGTATGACAGGCGAGG	3049
Db	889	GTAACACAGACTTATCCGCTACGACGACCTGCTGTAACGAGTATGACAGGCGAGG	948
Qy	3050	TATGTAGCGGTGTACAGAGTTCCTGAAAGTGTGGCTTAACTACGCGCTACACTAGAAAGG	3109
Db	949	TATGTAGCG--CGTGCTACAGAGTTCCTGAAAGTGTGGCTTAACTACGCGCTACACTAGAAAGG	1004
Qy	3110	ACAGTATTGTGTAATCGCGCTCTGCTGAAGC	3140
Db	1005	ACAGTATTGTGTAATCGCGCTCTGCTGAAGC	1035
RESULT 7			
CB686151/c			
LOCUS			
DEFINITION			
Bn01b_02008 A			
Bn01b_AAPC_ECORC transgenic Brassica napus overexpressing BNCBFL7 c			
onstitutively_frost_tolerant Brassica napus cDNA clone Bn01b_02008,			
mRNA sequence.			
CB686151			
CB686151.1 GI:29689876			
EST.			
Brassica napus (rape)			
Brassica napus			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;			
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.			
1 (bases 1 to 925)			
Singh, J., Allard, G., Tinker, N., Robert, L., Lacroix, C., De Moors, A.,			
Chagnon, J., Farah, S., Couroux, P. and Hattori, J.			
Expressed Sequence Tags from constitutively frost tolerant			
transgenic Brassica napus overexpressing BNCBFL7			
Unpublished (2002)			
Contact: Singh, J.A.			
Eastern Cereal and Oilseed Research Centre			
Agriculture and Agri-food Canada			
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A			
OC6, Canada			
Tel: (613) 759-1662			
Fax: (613) 759-1701			
Email: singhja@agr.gc.ca.			
Location/Qualifiers			
1-925			
/organism="Brassica napus"			
FEATURES			
source			

ORIGIN

Query Match		20.7%;	Score 896.2;	DB 6;	Length 925;
Best Local Similarity		98.3%;	Pred. No. 7.2e-197;		
Matches		909;	Conservative	6;	Mismatches 9; Indels 1; Gaps 1;
Qy	2220	TTTGTTCCTTTAGTAGAGGTTAATTTTCGAGCTTGGCGTAAATCATGTGTATAGCTGTTTC	2279		
Db	924	TTTGTTCCTTTAGTAGAGGTTAATTTTCGCGCTAATCATGTGTATAGCTGTTT-	866		
Qy	2280	CTGTGTGAATTTGTTATCCGCTCAAAATTCACACAACATACGAGCCGGAAGCATAAAGT	2339		
Db	865	CTGTGTGAATTTGTTATCCGCTCAAAATTCACACAACATACGAGCCGGAAGCATAAAGT	806		
Qy	2340	GTAAGAGCTTGGGTGTCCTTAATGAGTGAGCTAACTCAATTAATTTGCGTTGCGCTCACTGC	2399		
Db	805	GTAAGAGCTTGGGTGTCCTTAATGAGTGAGCTAACTCAATTAATTTGCGTTGCGCTCACTGC	746		
Qy	2400	CCGCTTTTCAGTCGGGAAAACCTGTGTCGAGCTGCATTAAATGATGGCCAAACGCGCGG	2459		
Db	745	CCGCTTTTCAGTCGGGAAAACCTGTGTCGAGCTGCATTAAATGATGGCCAAACGCGCGG	686		
Qy	2460	GGAGAGCGGTTTCGCTATTTCGGCGCTCTTCGGCTTCTCCGCTCACTGACTCGTGCCT	2519		
Db	685	GGAGAGCGGTTTCGCTATTTCGGCGCTCTTCGGCTTCTCCGCTCACTGACTCGTGCCT	626		
Qy	2520	CGGTCTGTTTCGGCTGCGCGAGCGGTATAGCTCACTCAAAAGCGGTAATACGGTTATCCA	2579		
Db	625	CGGTCTGTTTCGGCTGCGCGAGCGGTATAGCTCACTCAAAAGCGGTAATACGGTTATCCA	566		
Qy	2580	CAGAAATCAGGGGATAACGACGAAAGACATGTGAGCAAAAGGCCAGCAAGGCCACGAA	2639		
Db	565	CAGAAATCAGGGGATAACGACGAAAGAACATGTGAGCAAAAGGCCAGCAAGGCCACGAA	506		
Qy	2640	ACCGTAAAGAGCGCGGTTGCTGGCGTTTTCATAGGCTCCGCCCTTCAACGAGCATC	2699		
Db	505	ACCGTAAAGAGCGCGGTTGCTGGCGTTTTCATAGGCTCCGCCCTTCAACGAGCATC	446		
Qy	2700	ACAAAATTCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACGAG	2759		
Db	445	ACAAAATTCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACGAG	386		
Qy	2760	CGTTTCCCGCTGGAGCTCCCTCGTGGCTCTCTCGTTCCGACCTCGCGCTTACCGGAT	2819		
Db	385	CGTTTCCCGCTGGAGCTCCCTCGTGGCTCTCTCGTTCCGACCTCGCGCTTACCGGAT	326		
Qy	2820	ACCTGTCCGCTTCTTCCCTTCGGGAAGCGTGGCGCTTCTCAATGCTCACTGCTAGGT	2879		
Db	325	ACCTGTCCGCTTCTTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCAGCTGTAGGT	266		
Qy	2880	ATCTCAGTTTCGGTGTAGTGTGTTTCCTCAAGCTGGCTGTGTGTCAGCAAGACCCCGTTC	2939		
Db	265	ATCTCAGTTTCGGTGTAGTGTGTTTCCTCAAGCTGGCTGTGTGTCAGCAAGACCCCGTTC	206		
Qy	2940	AGCCCGAGCGCTGCGCTTATCCGCTAATCTGCTTTCGAGTCCCAACCCGCTGAAGACAG	2999		
Db	205	AGCCCGAGCGCTGCGCTTATCCGCTAATCTGCTTTCGAGTCCCAACCCGCTGAAGACAG	146		
Qy	3000	ACTTATCGCACTGGCAGCAGCCACTGTGTAAACGAGATTAGCAGAGGCTATGTAGGCG	3059		

Db 145 ACTTATCCCACTGGGACGACCCACTGCTTAACAGATTATACAGAGCGAGGTATGAGCG 86

QY 3060 GTGCTACAGAGTTCTTGAAGTGGTGGCTTAACCTACGCTACAGGACAGTATTG 3119

Db 85 GTGCTACAGAGTTCTTGAAGTGGTGGCTTAACCTACGCTACAGGACAGTATTG 26

QY 3120 GTATCTGGCTCTGCTGAAGCCAGT 3144

Db 25 GTATCTGGCTCTGCTGAAGCCAGT 1

RESULT 8

CV983341

LOCUS UMC-bof_OA01-002-506.Ovarian_Follicle_bof Bos taurus CDNA 3', mRNA

DEFINITION CV983341 951 bp linear EST 30-NOV-2004

ACCESSION CV983341

VERSION CV983341.1

KEYWORDS GI:56144062

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

1 (bases 1 to 951)

Prather,R.S., Antoniou,E., Garverick,H.A., Green,J.A., Lucy,M.C., Roberts,R.M., Smith,M.F. and Youngquist,R.S.

USDA Grant NRI-2002-03476: Bovine ESTs: Focus on Female Reproduction

Unpublished (2002)

Contact: DNA Core Facility (Bovine Project)

Animal Science - RS Prather

University of Missouri-Columbia

M616 Medical Sciences Bldg., Columbia, MO 65212, USA

Tel: (573)882-0428

Fax: (573)884-5552

Email: bovine@net.missouri.edu

POLYA=No.

Location/Qualifiers

1..951

/organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"

/dev_stage="Ovarian Follicle"

/clone_lib="bof"

/note="Vector: pSPORT1; Funding: The production of ESTs submitted in this project was funded by USDA Grant MRI-2002-03476 entitled 'Bovine ESTs: Focus on Female Reproduction' to RS Prather (Primary Investigator), E Antoniou, HA Garverick, JA Green, MC Lucy, RM Roberts, MF Smith and RS Youngquist. Genetic Source: Heifers for the project were purchased from Circle A Ranch, Iberia, MO (<http://www.circlearanch.com/home.html>). These heifers, while not registered have known Angus pedigrees going back at least 4 generations. Samples collected: The samples consisted of the following: germinal vesicle-stage oocytes; in vitro derived embryos (2-cell, morula, blastocyst and nuclear transfer blastocyst); in vivo corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian follicles (days 0, non-recruited, recruited, early selected and preovulatory); oviduct (days 0, 3 and 5); endometrium (days 5, 8, 14, 16, 18 and 35); and placenta/embryo from day 35 conceptuses. Expanded descriptions of how the tissues were collected can be found at the following URL: <http://genome.rnet.missouri.edu/Bovine/Methods.html>. Library construction (Standard Protocol): All procedures have been described in detail elsewhere (Soares et al., 1994; Bonaldo et al., 1996; Jiang et al., 2001). Total cellular RNA from each sample was isolated by using STAT-60 reagent (Tel-Test, Friendswood, TX) and the POLY(A)+ RNA was obtained by two rounds of purification

with the Oligotex mRNA isolation kit (Qiagen) according to the manufacturer's instructions. The libraries were constructed essentially as described by the manufacturer's instructions provided with the SuperScript Plasmid System (Invitrogen, cat. no. 18248-013). Briefly, 1mcg of poly(A)+ RNA was annealed at c37 degrees with 10mcg of NotI-tag-dt18 oligonucleotide (GCTGCTCGCGCGC-tag-T18) and reverse transcribed at c37 degrees with SuperScript II (Invitrogen) reverse transcriptase (Jiang et al., 2001). The 'tag' represents a tissue/stage-specific ten-base sequence identifier (<http://genome.uiowa.edu/pubsoft/software.html>) present in the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and RNase H. After second strand synthesis, the double-stranded cDNAs were ligated to SalI adapters (Invitrogen-Life Technologies) and digested with NotI. The cDNAs were size selected by passage through cDNA size fractionation columns (Invitrogen-Life Technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and SalI sites of the pCMV-SPORT6 vector (Invitrogen). After ligation of the inserts, the plasmids were electroporated into DH10B bacteria. Library Construction (PCR Protocol): The amount of mRNA that was recovered from oocytes and embryos was quite limiting and was not sufficient for library production with the standard protocol. Therefore, PCR-based protocol was utilized for producing libraries from sources in which the amount of extracted mRNA was small (oocytes and embryos). Poly-A RNA was isolated by using the MicroPoly(A) Pure kit from Ambion (cat. # 1918). The mRNA was reverse transcribed with a NotI-tag-dt18 oligonucleotide and a SMART oligonucleotide (Clontech) modified to contain a SalI site to generate full-length cDNA with a sequence complementary to the SMART oligonucleotide. Sequences within the SMART and dt oligonucleotides were used as primers to amplify the cDNAs by PCR with pfu turbo polymerase (Stratagene). The resulting PCR products were purified digested with NotI and SalI and size fractionated by using Chroma Spin-1000 columns (Clontech). Purified cDNA from each PCR reaction was quantitated and mixed on an equimolar basis for ligation into the pCMV-SPORT6 vector. Preliminary Library Characterization: randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (~4 96-well plates) to confirm library quality (e.g. the presence of short polyA+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.) and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. After production of the libraries, equal numbers of recombinants from each library were pooled to produce a single mixed library (mega-library) for more extensive sequencing. Bioinformatics work was performed by GK Springer's bioinformatics group in Computer Science at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core Facility at: bovine@net.missouri.edu. Bonaldo MF, Lennon G, Soares MB. Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res. 1996; 6:791-806. Jiang H, Bivens NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ, Springer GK, Didiion BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(A) tails. Biotechniques 31:38-42. Soares MB, MF Bonaldo, P Jelene, L Su, L Lawton, A Efstratiadis, 1994. Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci, 91:9228-9232. TAG_TISSUE=Ovarian Follicle

[illegible]

RESULT	9
CF269652	
LOCUS	
DEFINITION	CF269652 1073 bp mRNA linear EST 13-AUG-2003 Fycoldb844 fragilariopsis cylindrus SMART cDNA library (Clontech) Fragilariopsis cylindrus cDNA clone Antarctic 5', mRNA sequence

Db 361 CTATAAGATACAGGCGTTTCCCGCTGGAAGCTCCCTGCTGCGCTCTCTCTGCGAC 420
Qy 2804 CTGCGGCTTACCGGATACCTGTCGCGCTTCTCTCTGCGGAGCGTGGCGCTTCTCAA 2863
Db 421 CTGCGGCTTACCGGATACCTGTCGCGCTTCTCTCTGCGGAGCGTGGCGCTTCTCAT 480
Qy 2864 TGCTCAGCGCTAGGATCTCAGTTCCGCTGAGTGTGCTCTCTCAAGCTGGCGCTGTG 2923
Db 481 AGCTCAGCGCTAGGATCTCAGTTCCGCTGAGTGTGCTCTCTCAAGCTGGCGCTGTG 540
Qy 2924 CACGAACCCCGCTTACGCGCGAGCGCTGCGCGCTTATCCGCTAATCTGCTTGTAGTCC 2983
Db 541 CACGAACCCCGCTTACGCGCGAGCGCTGCGCGCTTATCCGCTAATCTGCTTGTAGTCC 600
Qy 2984 AACCCGGTATAGACAGCTTATCCGCTGAGTGTGCTCTCTCAAGCTGGCGCTGTG 3043
Db 601 AACCCGGTATAGACAGCTTATCCGCTGAGTGTGCTCTCTCAAGCTGGCGCTGTG 660
Qy 3044 GCGAGGTATGAGCGGCTGTACAGAGTCTTGAAGTGTGCGCT--AACTACGCGCTACA 3101
Db 661 GCGAGGTATGAGCGGCTGTACAGAGTCTTGAAGTGTGCGCTTAACTACGCGCTACA 720
Qy 3102 CTAGAAGACA-GTATTGTGATCT-GCGCTCTCTGAAGCC---AGTTACCTTCGAAA 3156
Db 721 CTAGAAGACAANGTATTGTGATCTGCGCTCTCTGAGAGCCAGNTTACGNTTCGAAA 780
Qy 3157 AAGAGTTGTGATCTTGTATCCGCGAGCAACCAACCGCTGAGCGGTGTTTTTGT 3216
Db 781 AAGAGTTGTGATCTTGTATCCGCGAGCAACCAACCGCTGAGCGGTGTTTTTGT 840
Qy 3217 TTCAAGCAGCAGATTAAGCGCGAGCAACCAACCGCTGAGCGGTGTTTTTGT 3276
Db 841 TTCAAGCAGCAGATTAAGCGCGAGCAACCAACCGCTGAGCGGTGTTTTTGT 900
Qy 3277 TACGGGTCTGACCTCAGTGTGAACGAAACTCAAGTTAAGGATTTTGTCTAGCGG 3336
Db 901 TACGGGTCTGACCTCAGTGTGAACGAAACTCAAGTTAAGGATTTTGTCTAGCGG 960
Qy 3337 ATACATATTGAATGATTTAGAAATAACAAA 3371
Db 961 ATACCTGANAATGCTTTTAATAATATGACAAA 995

RESULT 10
CL076016
LOCUS
DEFINITION
CH216-138F20, RM1.1 CH216 Xenopus tropicalis genomic clone
CL076016
CL076016.1 GI:40531929
GSS.

Accession
Version
Keywords
Source
Organism
Xenopus tropicalis (western clawed frog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Silurana.

REFERENCE
AUTHORS
Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E., and Wilson, R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)

TITLE
JOURNAL
COMMENT
Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: RM1 TAGCACTCACTATAGGAGA
Class: BAC ends
High quality sequence start: 11
High quality sequence stop: 810.
Location/Qualifiers
1. .885

FEATURES
Source

/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-138F20"
/sex="male"
/cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/notes="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"

ORIGIN

Query Match 19.7%; Score 854.4; DB 10; Length 885;
Best Local Similarity 99.1%; Pred. No. 3.7e-187;
Matches 869; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
Qy 2288 AATTGTTATCGGCTCAATTCACACATACGAGCCGGAAGCATAAAGTGTAAAGCC 2347
Db 5 AATTGTTATCGGCTCAATTCACACATACGAGCCGGAAGCATAAAGTGTAAAGCC 64
Qy 2348 TGGGGTGCCCTAATGAGTGAGCTAACTACATTAATTCGCTTCACCTGCCGCTTTC 2407
Db 65 TGGGGTGCCCTAATGAGTGAGCTAACTACATTAATTCGCTTCACCTGCCGCTTTC 124
Qy 2408 CAGTCGGGAAACCTGTCGCCAGCTGCAATTAATGAAATCGGCCAACCGCGGGAGAGCC 2467
Db 125 CAGTCGGGAAACCTGTCGCCAGCTGCAATTAATGAAATCGGCCAACCGCGGGAGAGCC 184
Qy 2468 GGTTCGGTATTCGGGCGCTCTTCGCTTCCTGCTCACTGACTCGCTGCGCTGCTTTC 2527
Db 185 GGTTCGGTATTCGGGCGCTCTTCGCTTCCTGCTCACTGACTCGCTGCGCTGCTTTC 244
Qy 2528 CGGCTCGGCGAGCGGTATCAGCTCACTCAAGGCGGTATACGTTATCCACAGATCA 2587
Db 245 CGGCTCGGCGAGCGGTATCAGCTCACTCAAGGCGGTATACGTTATCCACAGATCA 304
Qy 2588 GGGGATAACGCGAGGAAAGCAATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAA 2647
Db 305 GGGGATAACGCGAGGAAAGCAATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAA 364
Qy 2648 AAGCGCGGTGCTGCGGCTTTTTCATAGGCTCGGCGCTCGGCGCTCGGCGCTCGGCGCT 2707
Db 365 AAGCGCGGTGCTGCGGCTTTTTCATAGGCTCGGCGCTCGGCGCTCGGCGCTCGGCGCT 424
Qy 2708 CGACGCTCAAGTCAGAGGTGGCGAAACCGGACAGGACTATAAAGATACAGGCGTTTCCC 2767
Db 425 CGACGCTCAAGTCAGAGGTGGCGAAACCGGACAGGACTATAAAGATACAGGCGTTTCCC 484
Qy 2768 CTTGGAAGCTCCTCGTGGCTCTCTCTGTTCCGACCTGCGCTTACCGGATACCTGTCC 2827
Db 485 CTTGGAAGCTCCTCGTGGCTCTCTCTGTTCCGACCTGCGCTTACCGGATACCTGTCC 544
Qy 2828 GCCTTTCTCCTTCGGGAGCGTGGCGCTTTCTCAATGCTCAGCTGTAGTATCTCAGT 2887
Db 545 GCCTTTCTCCTTCGGGAGCGTGGCGCTTTCTCAATGCTCAGCTGTAGTATCTCAGT 604
Qy 2888 TCGGCTGTAGTGTGCTGCTCCAGCTGGGCTGTGTGCAAGAACCCCGCTTCAGCGCCGAC 2947
Db 605 TCGGCTGTAGTGTGCTGCTCCAGCTGGGCTGTGTGCAAGAACCCCGCTTCAGCGCCGAC 664
Qy 2948 CGCTGCGCTTATCCGCTAACCTATCTGTTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT 3007
Db 665 CGCTGCGCTTATCCGCTAACCTATCTGTTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT 724
Qy 3008 CCACTGGGAGCAGCTTGTAAACAGATTAACAGAGCGGATGATGAGCGGTGCTACA 3067
Db 725 CCACTGGGAGCAGCTTGTAAACAGATTAACAGAGCGGATGATGAGCGGTGCTACA 784
Qy 3068 GAGTTCCTGAAGTGTGGCTTAACCTACGCTACACTAGAGGAGCAGTATTGTTGTTATCTGC 3127
Db 785 GAGTTCCTGAAGTGTGGCTTAACCTACGCTACACTAGAGGAGCAGTATTGTTGTTATCTGC 844
Qy 3128 GCTCTGCTGAAGCCAGTTACCTTTTCGGAAGAGGTTG 3164

```
Db      845  GCTCTGCTGAAG-CAGTTACCTTCGGAAGAGAGTGG 880
|||||
DR046031      1195 bp      mRNA      linear      EST 02-JUN-2005
LOCUS      FP-8 F02_SEQ cDNA library of Phaeosphaeria nodorum grown on wheat
DEFINITION      cell_walls Phaeosphaeria nodorum cDNA, mRNA sequence.
ACCESSION      DR046031
VERSION      DR046031.1 GI:86909867
KEYWORDS      EST.
SOURCE      Phaeosphaeria nodorum
ORGANISM      Phaeosphaeria nodorum
              Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
              Pleosporales; Phaeosphaeriaceae; Phaeosphaeria.
REFERENCE      1 (bases 1 to 1195)
AUTHORS      Bindschedler,L.V., Cooper,R.M., Thomas,S.W., Madrid,M.P. and
              Oliver,R.P.
              cDNA library of Phaeosphaeria nodorum grown on wheat cell walls
              Unpublished (2005)
              Contact: Richard Oliver
              Australian Centre for Necrotrophic Fungal Pathogens (ACNFP)
              Murdoch University
              South Street, Murdoch, W.A 6150, Australia
              Tel: +0893607404
              Email: roliver@murdoch.edu.au.
FEATURES      location/Qualifiers
              source
              1..1195
              /organism="Phaeosphaeria nodorum"
              /mol_type="mRNA"
              /db_xref="taxon:13684"
              /clone_lib="cDNA library of Phaeosphaeria nodorum grown on
              wheat cell walls"

ORIGIN
Query Match      19.7%; Score 853.6; DB 8; Length 1195;
Best Local Similarity 97.2%; Pred. No. 5.9e-187;
Matches 902; Conservative 0; Mismatches 19; Indels 7; Gaps 3;

QY      2210  AGCTCAGCTTTTGTTCCTTTAGTCAGGGTTAAATTCGAGCTTCGGCGTAATCATGGTCA 2269
Db      164  AGCTCCAGCTTTTGTTCCTTTAGTCAGGGTTAAATTCGAGCTTCGGCGTAATCATGGTCA 223
QY      2270  TAGCTGTTTCCTGTGTGAAATTTATCCGCTCACAAATCCACAAACATACAGCCGGA 2329
Db      224  TAGCTGTTTCCTGTGTGAAATTTATCCGCTCACAAATCCACAAACATACAGCCGGA 283
QY      2330  AGCATAAAGTGTAAGCCTGGGGTGCTTAATGAGTGAGCTAATCATTAATTGGGTTG 2389
Db      284  AGCATAAAGTGTAAGCCTGGGGTGCTTAATGAGTGAGCTAATCATTAATTGGGTTG 343
QY      2390  CGCTCATCTCCGCTTTTCAGTCGGGAACCTGTGTCGACGTGCATTAATGAATCGGC 2449
Db      344  CGCTCATCTCCGCTTTTCAGTCGGGAACCTGTGTCGACGTGCATTAATGAATCGGC 403
QY      2450  CAAACGCGGGGAGAGCGGTTTGCTATTGGCGCTCTTCGCGCTTCCTCGCTCACTGAC 2509
Db      404  CAAACGCGGGGAGAGCGGTTTGCTATTGGCGCTCTTCGCGCTTCCTCGCTCACTGAC 463
QY      2510  TCCTCGCTCGCTCGCTTCGCTTCGCGGAGCGGTATCAGCTCACTCAAAGCGGTAATA 2569
Db      464  TCCTCGCTCGCTCGCTTCGCTTCGCGGAGCGGTATCAGCTCACTCAAAGCGGTAATA 523
QY      2570  CGGTTATCCACAATCAGGGTAACCGCAGGAAGAACATGTGAGCAAAAGCCAGCAA 2629
Db      524  CGGTTATCCACAATCAGGGTAACCGCAGGAAGAACATGTGAGCAAAAGCCAGCAA 583
QY      2630  AAGCCAGGAACCGTAAAAAGCGCGGTTGCTCGCGTTTTTCATAGGCTCCGCCCCCT 2689
Db      584  AAGCCAGGAACCGTAAAAAGCGCGGTTGCTCGCGTTTTTCATAGGCTCCGCCCCCT 643
QY      2690  GACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAA 2749
```

```
Db      644  GACGAGCATCACAAAATGACGCTCAAGTCAGAGTGGCGAAACCGACAGGACTATAA 703
QY      2750  AGATACCAGCGGTTTCCCCCTCGGAAGCTCCCTCGTGGCTCTCTCTGTTTCGACCTGCCG 2809
Db      704  AGATACCAGCGGTTTCCCCCTCGGAAGCTCCCTCGTGGCTCTCTCTGTTTCGACCTGCCG 763
QY      2810  CTTACCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAGCGTGGGCTTTTCTCAATGCTCA 2869
Db      764  CTTACCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAGCGTGGGCTTTTCTCAATGCTCA 823
QY      2870  CGCTGTAGGTATCTCAGTTCGTTGAGTGTGCTTCGCTCCAAAGCTGGGCTGTGTGCACGAA 2929
Db      824  CGCTGTAGGTATCTCAGTTCGTTGAGTGTGCTTCGCTCCAAAGCTGGGCTGTGTGCACGAA 883
QY      2930  CCCCCCTTCAGCCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGTAGTCAACCCG 2989
Db      884  CCCCCCTTCAGCCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGTAGTCAACCCG 943
QY      2990  GTAAGACAGCACTTATCGCACTGGCAGCAGCCACTGGTAACAGGATTCAGAGCGGAGG 3049
Db      944  GTAAGA-ACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTCAGAGCGGAGG 1002
QY      3050  TATGTAGCGGTGCTACAGAGTTCCTCGAAGTGGTGGCTTAACCTACGCTACACATAGAAGG 3109
Db      1003  TATGTAG--CGTGTCTACAGAGTTCCTCGAAGTGGTGGC---CTACTAGGCTACCTAGAG 1056
QY      3110  ACAGTATTGGTATCTCGGCTCTGCTGA 3137
Db      1057  AACAGTATTGGTATCTCGGCTCTGCTGA 1084

RESULT 12
LOCUS      CX012952
DEFINITION      ioe2d12.bi Whole Heart Library (DOGEST5) Canis familiaris cDNA,
              mRNA sequence.
ACCESSION      CX012952
VERSION      CX012952.1 GI:56395363
KEYWORDS      EST.
SOURCE      Canis familiaris (dog)
ORGANISM      Canis familiaris
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
              Canis.
REFERENCE      1 (bases 1 to 875)
AUTHORS      Balija,V.S., Nasciminto,L.U. and McCombie,W.R.
TITLE      ESTs from Canis familiaris whole heart (dog)
JOURNAL      Unpublished (2004)
COMMENT      Contact: W. Richard McCombie
              Lita Annenberg Hazen Genome Sequencing Center
              Cold Spring Harbor Laboratory
              PO Box 100, Cold Spring Harbor, NY 11724, USA
              Tel: 516 367 8884
              Fax: 516 367 8874
              Email: mcombie@cshl.org
              location/Qualifiers
              source
              1..875
              /organism="Canis familiaris"
              /mol_type="mRNA"
              /db_xref="taxon:9615"
              /sex="Unknown"
              /dev_stage="3 month old normal canine"
              /lab_host="X110 Gold"
              /clone_lib="Whole Heart Library (DOGEST5)"
              /note="Organ: Heart; Vector: pBluescript II SK; Site: 1:
              EORI; Site 2: XhoI; Library constructed using pluescript
              XR kit from Stratagene. Cloned cDNA was size selected
              between 1-3 kb. Mark Haskins VMD, PhD, pathology and
              Medical Genetics, School of Veterinary Medicine,
              University of Pennsylvania, 3800 Spruce Street,
              Philadelphia, PA 19104-6051"

ORIGIN
```

Query Match 19.7%; Score 852; DB 8; Length 875;
 Best Local Similarity 98.8%; Pred. No. 1.3e-186;
 Matches 858; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2435 CATTAAATGAATCGGCAACGCGGGAGAGCGGTTGCGTATTTGGCGCTCTTCCGCT 2494
 Db 8 CTTTAAATGAATCGGCAACGCGGGAGAGCGGTTGCGTATTTGGCGCTCTTCCGCT 67

QY 2495 TCCTCGCTCACTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 2554
 Db 68 TCCTCGCTCACTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 127

QY 2555 TCAAGGCGGTAAATACGTTATCCACAGAAATCAGGGGATACGAGGAAAGAAATGTGA 2614
 Db 128 TCAAGGCGGTAAATACGTTATCCACAGAAATCAGGGGATACGAGGAAAGAAATGTGA 187

QY 2615 GCAAAAGCCAGCAAAAGCCAGGAAACCGTAAAGGCGGTTGCTGGCGCTTTTCCAT 2674
 Db 188 GCAAAAGCCAGCAAAAGCCAGGAAACCGTAAAGGCGGTTGCTGGCGCTTTTCCAT 247

QY 2675 AGGCTCCGCCCCCTGACGACATCACAAAATCGAGCTCAAGTCAGAGTGGCGAAC 2734
 Db 248 AGGCTCCGCCCCCTGACGACATCACAAAATCGAGCTCAAGTCAGAGTGGCGAAC 307

QY 2735 CCGACAGGACTATAAGATACAGGCGGTTTCCCTTGAAGCTCCCTCGCTCGCTCTCCT 2794
 Db 308 CCGACAGGACTATAAGATACAGGCGGTTTCCCTTGAAGCTCCCTCGCTCGCTCTCCT 367

QY 2795 GTTCCGACCTGCGCTTACCGGATACCTGTGCGGCTTTCCCTTCCGGAAGCGTGGC 2854
 Db 368 GTTCCGACCTGCGCTTACCGGATACCTGTGCGGCTTTCCCTTCCGGAAGCGTGGC 427

QY 2855 CTTTCTCAATGCTACGCTGAGTACTCAGTTGCGGTGAGTGCCTGCTCAAGCTG 2914
 Db 428 CTTTCTCAATGCTACGCTGAGTACTCAGTTGCGGTGAGTGCCTGCTCAAGCTG 487

QY 2915 GGCTGTGTGACGAACCCCGTTTCCGCGACCGCTGCGCTTTATCCGGTAACTATCGT 2974
 Db 488 GGCTGTGTGACGAACCCCGTTTCCGCGACCGCTGCGCTTTATCCGGTAACTATCGT 547

QY 2975 CTTGAGTCCAAACCGGTAAAGACAGCTATTCGCACTGGCAGGACCTGTTAAACAG 3034
 Db 548 CTTGAGTCCAAACCGGTAAAGACAGCTATTCGCACTGGCAGGACCTGTTAAACAG 607

QY 3035 ATTAGCAGAGGAGTATGAGGCGGTGCTACAGATTTCTTGAAGTGGTGGCTTAAC 3094
 Db 608 ATTAGCAGAGGAGTATGAGGCGGTGCTACAGATTTCTTGAAGTGGTGGCTTAAC 667

QY 3095 GGCTTACACTAGAAGCAGATATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTCGGA 3154
 Db 668 GGCTTACACTAGAAGCAGATATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTCGGA 727

QY 3155 AAAAGAGTGGTAGCTCTTGAATCGGCAAAACCAACCGCTGAGCGGTGTTTGT 3214
 Db 728 AAAAGAGTGGTAGCTCTTGAATCGGCAAAACCAACCGCTGAGCGGTGTTTGT 787

QY 3215 GTTTGCAAGCAGCAGATTTACGCGCAGAAAGGATCTCAAGAGATCTTTGATCTTT 3274
 Db 788 GTTTGCAAGCAGCAGATTTACGCGCAGAAAGGATCTCAAGAGATCTTTGATCTTT 847

QY 3275 TCTACGGGCTGACGCTCAGTGGAAACG 3302
 Db 848 TCTACGGGCTGACGCTCAGTGGAAACG 875

RESULT 13
 AU081044 1163 bp mRNA linear EST 30-JUL-2002
 LOCUS AU081044 Oncorhynchus mykiss Kidney infected by infectious
 DEFINITION hematopoietic necrosis virus Oncorhynchus mykiss cDNA clone KB1,
 mRNA sequence.
 ACCESSION AU081044

AU081044.1 GI:6431392
 EST.
 Oncorhynchus mykiss (rainbow trout)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 REFERENCE
 1 (bases 1 to 1163)
 Kono T., Sakai M. and LaPatra S.E.
 Expressed Sequence Tag Analysis of Kidney and Gill Tissues from
 Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious
 Hematopoietic Necrosis Virus
 Mar. Biotechnol. 2 (5), 493-498 (2001)
 AUTHORS
 Contact: Masahiro Sakai
 Faculty of Agriculture
 Miyazaki University
 Miyazaki
 1-1 mishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192, Japan
 Email: m.sakai@cc.miyazaki-u.ac.jp.
 Location/Qualifiers
 1..1163
 /organism="Oncorhynchus mykiss"
 /mol_type="mRNA"
 /db_xref="taxon:8022"
 /clone="KB1"
 /tissue_type="kidney"
 /clone_lib="Oncorhynchus mykiss Kidney infected by
 infectious hematopoietic necrosis virus"
 /note="common name:rainbow trout ; infected by infectious
 hematopoietic necrosis virus"
 ORIGIN
 Query Match 19.0%; Score 822.2; DB 1; Length 1163;
 Best Local Similarity 99.5%; Pred. No. 1.2e-179;
 Matches 835; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 2210 AGCTCCAGCTTTTGTTCCTTTAGTGAGGTTTAAATTCGAGCTTGGCGTAAATCATGTCA 2269
 Db 326 AGCTCCAGCTTTTGTTCCTTTAGTGAGGTTTAAATTCGAGCTTGGCGTAAATCATGTCA 385

QY 2270 TAGCTGTTTCTGCTGTAATTTGTTATCCGCTCACAATTCACACATACGAGCCGGA 2329
 Db 386 TAGCTGTTTCTGCTGTAATTTGTTATCCGCTCACAATTCACACATACGAGCCGGA 445

QY 2330 AGCATAAAGTAAAGCTGGGCTGCTATAGTGAAGTAACTCAATTAATTCGCTG 2389
 Db 446 AGCATAAAGTAAAGCTGGGCTGCTATAGTGAAGTAACTCAATTAATTCGCTG 505

QY 2390 CGCTCACTGCGCTTTTCCAGTCGGGAAACCTGCTGCGAGCTGCAATTAATGAATCGGC 2449
 Db 506 CGCTCACTGCGCTTTTCCAGTCGGGAAACCTGCTGCGAGCTGCAATTAATGAATCGGC 565

QY 2450 CAACGCGGGAGAGCGGTTTGGTATTTGGGCGCTTCCGCTTCTCGCTCACTGAC 2509
 Db 566 CAACGCGGGAGAGCGGTTTGGTATTTGGGCGCTTCCGCTTCTCGCTCACTGAC 625

QY 2510 TCCTGCGCTGCGCTGCTTCCGCTGCGGAGCGGTATCAGTCACTCAAAAGCGGTAATA 2569
 Db 626 TCCTGCGCTGCGCTGCTTCCGCTGCGGAGCGGTATCAGTCACTCAAAAGCGGTAATA 685

QY 2570 CGGTTATCCACAGATCAGGGGATACGCAAGGAAAGCAATGTGAGCAAAAGCGCAGCAA 2629
 Db 686 CGGTTATCCACAGATCAGGGGATACGCAAGGAAAGCAATGTGAGCAAAAGCGCAGCAA 745

QY 2630 AAGGCCAGGAACCGTAAAGGCGGTTGCTGCGGTTTCCATAGGCTCCGCCCTCCCT 2689
 Db 746 AAGGCCAGGAACCGTAAAGGCGGTTGCTGCGGTTTCCATAGGCTCCGCCCTCCCT 805

QY 2690 GACGAGCATCAAAAATCGACGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAA 2749
 Db 806 GACGAGCATCAAAAATCGACGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAA 865

QY 2750 AGATACAGGCGTTTCCCTCGGAGCTCCCTCGTGGGCTCTCTGTTCCGACCTCGCG 2809

Db 866 AGATACCAGGCGTTTCCCTCCGGAAGTCCCTCGGCGCTCTCCTGTTCCGACCCCTGCCG 925
 QY 2810 CTTACCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCCTCAATGTCTCA 2869
 Db 926 CTTACCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCCTCAATGTCTCA 985
 QY 2870 CGCTGTAGGTATCTCAGTTCGGTGTAGGTGTCGCTCCAGCTCGGCTGTGTGTCACGAA 2929
 Db 986 CGCTGTAGGTATCTCAGTTCGGTGTAGGTGTCGCTCCAGCTCGGCTGTGTGTCACGAA 1045
 QY 2930 CCCCCGTTACCGCGACCGTGGCGCTTATCCGCTACCTATCGTCTTGATCTCAACCCG 2989
 Db 1046 -CCCCGTTACCGCGACCGTGGCGCTTATCCGCTACCTATCGTCTTGATCTCAACCCG 1104
 QY 2990 GTAAGACACGACTTATCCGCTACTGCGACGACCTGCTAATACAGATTAGCAGAGCGAG 3048
 Db 1105 GTAAGACACGACTTATCCGCTACTGCGACGACCTGCTAATACAGATTAGCAGAGCGAG 1163

RESULT 14
 CV984340
 LOCUS UMC-bov_0A02-010-e02 Oviduct bov Bos taurus CDNA 3', mRNA sequence.
 DEFINITION UMC-bov_0A02-010-e02 Oviduct bov Bos taurus CDNA 3', mRNA sequence.
 ACCESSION CV984340
 VERSION CV984340.1 GI:56145061
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.
 1 (bases 1 to 868)
 Prather, R.S., Smith, M.F. and Youngquist, R.S.
 Roberts, R.M., Smith, M.F. and Youngquist, R.S.
 USDA Grant NRI-2002-03476: Bovine ESTs: Focus on Female
 Reproduction
 Unpublished (2002)
 Contact: DNA Core Facility (Bovine Project)
 Animal Science - RS Prather
 University of Missouri-Columbia
 M616 Medical Sciences Bldg., Columbia, MO 65212, USA
 Tel: (573)882-0428
 Fax: (573)884-5552
 Email: bovine@net.missouri.edu
 POLYA=No.

FEATURES
 source
 1..868
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /clone_lib="bov"
 /note="Funding: The production of ESTs submitted in this project was funded by USDA Grant MRI-2002-03476 entitled 'Bovine ESTs: Focus on Female Reproduction' to RS Prather, E Antoniou, HA Garverick, JA Green, MC Lucy, RM Roberts, MF Smith and RS Youngquist. Genetic Source: Heifers for the project were purchased from Circle A Ranch, Iberia, MO (<http://www.circlea ranch.com/home.html>). These heifers, while not registered have known Angus pedigrees going back at least 4 generations. Samples collected: The samples consisted of the following: Germinal vesicle-stage oocytes; in vitro derived embryos (2-cell, morula, blastocyst and nuclear transfer blastocyst); in vivo blastocysts and conceptuses (days 8, 14, 16 and 18); corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian follicles (days 0, non-recruited, recruited, early selected and preovulatory); oviduct (days 0, 3 and 5); endometrium (days 5, 8, 14, 16, 18 and 35); and placenta/embryo from day 35 conceptuses. Expanded descriptions of how the tissues were collected can be found at the following URL: <http://genome.rnet.missouri.edu/Bovine/Methods.html>. Library construction (Standard Protocol): All procedures

have been described in detail elsewhere (Soares et al., 1994; Bonaldo et al., 1996; Jiang et al., 2001). Total cellular RNA from each sample was isolated by using STAT-60 reagent (Tel-Test, Friendswood, TX) and the poly(A)+ RNA was obtained by two rounds of purification with the Oligotex mRNA isolation kit (Qiagen) according to the manufacturer's instructions. The libraries were constructed by E. Ferguson and R. Woods essentially as described by the manufacturer's instructions provided with the SuperScript plasmid system (Invitrogen, cat. no. 18248-013). Briefly, 1mcg of poly(A)+ RNA was annealed at 37 degrees with 10mcg of NotI-tag-drl8 oligonucleotide (GTCGCTGGCGCGC-tag-118) and reverse transcribed at 42 degrees with Superscript II (Invitrogen) reverse transcriptase (Jiang et al., 2001). The 'tag' represents a tissue/stage-specific ten-base sequence identifier (<http://genome.uiowa.edu/pubsoft/software.html>) present in the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and RNase H. After second strand synthesis, the double-stranded cDNAs were ligated to SalI adapters (Invitrogen-Life Technologies) and digested with NotI. The cDNAs were size selected by passage through cDNA size fractionation columns (Invitrogen-Life Technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and SalI sites of the pCMV-SPORT6 vector (Invitrogen). After ligation of the inserts, the plasmids were electroporated into DH10B bacteria. Library Construction (PCR Protocol): The amount of mRNA that was recovered from oocytes and embryos was quite limiting and was not sufficient for library production with the standard protocol. Therefore, PCR-based protocol was utilized for producing libraries from sources in which the amount of extracted mRNA was small (oocytes and embryos). Poly-A RNA was isolated by using the MicroPoly(A) Pure kit from Ambion (cat. # 1918). The mRNA was reverse transcribed with a NotI-tag-drl8 oligonucleotide and a SMART oligonucleotide (Clontech) modified to contain a SalI site to generate full-length cDNA with a sequence complementary to the SMART oligonucleotide. Sequences within the SMART and dt oligonucleotides were used as primers to amplify the cDNAs by PCR with pfu turbo polymerase (Stratagene). The resulting PCR products were purified, digested with NotI and SalI and size fractionated by using Chroma Spin-1000 columns (Clontech). Purified cDNA from each PCR reaction was quantitated and mixed on an equimolar basis for ligation into the pCMV-SPORT6 vector. Preliminary Library Characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (-4 96-well plates) to confirm library quality [e.g. the presence of short polyA+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.] and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. After production of the libraries, equal numbers of recombinants from each library were pooled to produce a single mixed library (mega-library) for more extensive sequencing. Bioinformatics work was performed by GK Springer's Bioinformatics group (Spollen WG, Topinka CM, Khambati AA) in Computer Science at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core facility at: bovine@net.missouri.edu. Bonaldo MF, Lennon G, Soares MB. Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res, 1996; 6:791-806. Jiang H, Bivens NJ, Ries JB, Whitworth KM, Green JA, Forrester LJ, Springer GK, Dildon BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing

cdna libraries with fewer clones that contain long poly(dA) tails. Biotechniques 31:38-42. Soares MB, MF Bando, P Jellene, L Su, L Lawton, A Efstratiadis. 1994. Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci, 91:9228-9232.
TAG_ISSUE=Oviduct
TAG_SEQ=Not found"

ORIGIN

```
Query Match      19.0%; Score 821.2; DB 8; Length 868;
Best Local Similarity 98.6%; Pred. No. 1.9e-179;
Matches 848; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

Qy 2446 CGGCCAACCGCGGGAGAGCGGTTTGGCGATTGGCGCTCTCTCCGCTTCTCCGCTCCTCGCTCAC 2505
Db 2 CGGCCAACCGCGGGAGAGCGGTTTGGCGATTGGCGCTCTCTCCGCTTCTCGCTCAC 61

Qy 2506 TGACTCGCTGCGCTCGGTCGCTCGGCTCGCGGAGCGGTATCAGCTACTCAAAAGGCGGT 2565
Db 62 TGACTCGCTGCGCTCGGTCGCTCGGCTCGCGGAGCGGTATCAGCTACTCAAAAGGCGGT 121

Qy 2566 AATACGGTTATCCACAGATCAGGGGATAACGACAGGAAGAACATGTGAGCAAAAGGCCA 2625
Db 122 AATACGGTTATCCACAGATCAGGGGATAACGACAGGAAGAACATGTGAGCAAAAGGCCA 181

Qy 2626 GCAAAAGGCCAGGAACCGTAAAAAGCGCGCTTCTGCGCTTTTTCATAGGCTCCGCC 2685
Db 182 GCAAAAGGCCAGGAACCGTAAAAAGCGCGCTTCTGCGCTTTTTCATAGGCTCCGCC 241

Qy 2686 CCCTGACGAGCATCACAAAATCAGCGCTCAAGTCAGAGTGGCGAAACCGCAGCAGCT 2745
Db 242 CCCTGACGAGCATCACAAAATCAGCGCTCAAGTCAGAGTGGCGAAACCGCAGCAGCT 301

Qy 2746 ATAAGATACACAGCGTTTCCCTCGGAAGTCCCTCGTGGCTCTCTCTGTCGACCT 2805
Db 302 ATAAGATACACAGCGTTTCCCTCGGAAGTCCCTCGTGGCTCTCTCTGTCGACCT 361

Qy 2806 GCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGAAGCGTGGCGCTTCTCAATG 2865
Db 362 GCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAG 421

Qy 2866 CTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCTGCTCGCTCAAGCTGGCTGTGTGCA 2925
Db 422 CTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCTGCTCGCTCAAGCTGGCTGTGTGCA 481

Qy 2926 CGAACCCCGCTTCAGCGCCAGCCCTGCGCTTATCCGTTAATCATCTGTGAGTCCAA 2985
Db 482 CGAACCCCGCTTCAGCGCCAGCCCTGCGCTTATCCGTTAATCATCTGTGAGTCCAA 541

Qy 2986 CCGGTTAAGACACGACTTATGCGCACTGGCAGCAGCCACTGGTAAACAGGATTAGCAGAGC 3045
Db 542 CCGGTTAAGACACGACTTATGCGCACTGGCAGCAGCCACTGGTAAACAGGATTAGCAGAGC 601

Qy 3046 GAGGTATGTAGCGGCTCTACAGAGTCTTGAAGTGTGGCTTAATCAGGCTACACTAG 3105
Db 602 GAGGTATGTAGCGGCTCTACAGAGTCTTGAAGTGTGGCTTAATCAGGCTACACTAG 661

Qy 3106 AAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGAGTTGG 3165
Db 662 AAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGAGTTGG 721

Qy 3166 TAGCTCTTGATCCGGCAAAACAAACCCACCGCTGTAGCGGTGGTTTTTTTGTGTGCAAGCA 3225
Db 722 TAGCTCTTGATCCGGCAAAACAAACCCACCGCTGTAGCGGTGGTTTTTTTGTGTGCAAGCA 780

Qy 3226 GCAGATTACCGCGAAGAAAAGATCTCAAGAGATCTCTTGAATCTTTTCTACGGGCTC 3285
Db 781 GCAGATTACCGCGAAGAAAAGATCTCTCAAGAGATCTCTTGAATCTTTTCTACGGGCTC 839

Qy 3286 TGACGCTCAGTGGAAACGAAA 3305
Db 840 TGACGCTCAGTGGAAACGAAA 859
```

RESULT 15

AG332951

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

ORIGIN

Query Match

Best Local Similarity

Matches

917; Conservative

0; Mismatches

105; Indels

5; Gaps

3;

Qy

2245

TTCCAGCTTGGCGTAAATCATGTCATAGCTGTGTTCTCTGTGTGAAATTTGTTATCCGCTCAC

2304

Db

136

TGCAAGCTTGGCGTAAATCATGTCATAGCTGTGTTCTCTGTGTGAAATTTGTTATCCGCTCAC

195

Qy

2305

AATTCACACACATACGAGCCGAGCATAAAGTGTAAAGCTGGGTCCTTAATGAGT

2364

Db

196

AATTCACACACATACGAGCCGAGCATAAAGTGTAAAGCTGGGTCCTTAATGAGT

255

Qy

2365

GAGTAACCTACATTAATTTGCGTTCGCTACCTGCGGCTTTCAGTTCGGGAAACCTGTC

2424

Db

256

GAGTAACCTACATTAATTTGCGTTCGCTACCTGCGGCTTTCAGTTCGGGAAACCTGTC

315

Qy

2425

GTCCAGCTGCAATTAATGAATCGCCAAACGCGCGGGAGAGCGGTTTTCGTTATTTGGGCG

2484

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2006, 04:23:02 ; Search time 1282 Seconds
(without alignments)

Title: US-10-811-028A-1

Perfect score: 4331

Sequence: 1 cggtcgggcctctcgcta.....ttgatccctgcgccatcag 4332

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA: *

```

1: /cgn2_6/prodata1/1na/1 COMB.seq.*
2: /cgn2_6/prodata1/1na/5 COMB.seq.*
3: /cgn2_6/prodata1/1na/6 COMB.seq.*
4: /cgn2_6/prodata1/1na/8 COMB.seq.*
5: /cgn2_6/prodata1/1na/8 COMB.seq.*
6: /cgn2_6/prodata1/1na/8 COMB.seq.*
7: /cgn2_6/prodata1/1na/8 COMB.seq.*
8: /cgn2_6/prodata1/1na/8 COMB.seq.*
9: /cgn2_6/prodata1/1na/8 COMB.seq.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1845.4	42.6	8349	3	US-09-186-003-16	Sequence 16, Appl
2	1719	39.7	5707	2	US-08-472-803B-8	Sequence 8, Appl
3	1586.2	36.6	4644	3	US-09-479-123-19	Sequence 19, Appl
4	1586.2	36.6	4644	3	US-09-484-997-19	Sequence 19, Appl
5	1586.2	36.6	4644	3	US-09-481-355-19	Sequence 19, Appl
6	1586.2	36.6	4644	3	US-09-481-283-19	Sequence 19, Appl
7	1586.2	36.6	4644	3	US-09-455-659A-19	Sequence 19, Appl
8	1586.2	36.6	4644	3	US-09-484-996-19	Sequence 19, Appl
9	1586.2	36.6	4644	3	US-09-479-123-19	Sequence 19, Appl
10	1586.2	36.6	4644	3	US-09-484-317A-19	Sequence 19, Appl
11	1586.2	36.6	4644	3	US-09-276-820A-19	Sequence 19, Appl
12	1586.2	36.6	5247	3	US-09-479-123-20	Sequence 20, Appl
13	1586.2	36.6	5247	3	US-09-484-997-20	Sequence 20, Appl
14	1586.2	36.6	5247	3	US-09-481-355-20	Sequence 20, Appl
15	1586.2	36.6	5247	3	US-09-481-283-20	Sequence 20, Appl
16	1586.2	36.6	5247	3	US-09-455-659A-20	Sequence 20, Appl
17	1586.2	36.6	5247	3	US-09-484-996-20	Sequence 20, Appl
18	1586.2	36.6	5247	3	US-09-479-123-20	Sequence 20, Appl
19	1586.2	36.6	5247	3	US-09-484-317A-20	Sequence 20, Appl
20	1586.2	36.6	5247	3	US-09-276-820A-20	Sequence 20, Appl
21	1586.2	36.6	5314	3	US-09-479-123-27	Sequence 27, Appl
22	1586.2	36.6	5314	3	US-09-484-997-27	Sequence 27, Appl
23	1586.2	36.6	5314	3	US-09-481-355-27	Sequence 27, Appl
24	1586.2	36.6	5314	3	US-09-481-283-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1

```

US-09-186-002-16
; Sequence 16, Application US/09186002B
; Patent No. 6489542
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Method
; TITLE OF INVENTION: delta-Endotoxins
; FILE REFERENCE: 38-21(13547) US Pat
; CURRENT APPLICATION NUMBER: US/09/18
; CURRENT FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 16
; LENGTH: 8349
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: gene
; LOCATION: (3666)..(5573)
; OTHER INFORMATION: completely synth
US-09-186-002-16

```

	Query Match	42.6%	Score 1845.4	DB 3	Length 8349	
	Best Local Similarity	92.6%	Pred. No. 6.4e-102			
	Matches 1983	Conservative	0	Mismatches 101	Indels 57	Gaps 2
Qy	2249	AGCTTGGCGTAATCATGGTTCATAGCTGTTTCCCTGTGTGAAATGTTATCCGCTCACAAT	2308			
Db	5909	AGCTTGGCGTAATCATGGTTCATAGCTGTTTCCCTGTGTGAAATGTTATCCGCTCACAAT	5968			
Qy	2309	CCACACACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGC	2368			
Db	5969	CCACACACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGC	6028			
Qy	2369	TAACTCACATTAATTCGGTTGCGCTCACCTGCCGCTTTCACAGTCGGGAAACCTGTGCTGC	2428			
Db	6029	TAACTCACATTAATTCGGTTGCGCTCACCTGCCGCTTTCACAGTCGGGAAACCTGTGCTGC	6088			
Qy	2429	CAGCTGCATTAATGAATCCGCCAACCGGGGAGAGCGGTTTGGGTATTTGGCGCGCTCT	2488			
Db	6089	CAGCTGCATTAATGAATCCGCCAACCGGGGAGAGCGGTTTGGGTATTTGGCGCGCTCT	6148			
Qy	2489	TCGCGTCTCTCGCTCACTGACTCGCTCGCTCGGTCGGTTCGGTTCGGCGGAGCGGTATCA	2548			
Db	6149	TCGCGTCTCTCGCTCACTGACTCGCTCGCTCGGTCGGTTCGGTTCGGCGGAGCGGTATCA	6208			

Qy 2549 GCTCACTCAAAGGCGGTAAATACGGTTATTCACAGAAATCAGGGGATAACGACGAGAAAGAAC 2608
 Db |||||
 Qy 6209 GCTCACTCAAAGGCGGTAAATACGGTTATTCACAGAAATCAGGGGATAACGACGAGAAAGAAC 6268
 Db |||||
 Qy 2609 ATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAAAAGGCGGCTTGTCTGGCGTTT 2668
 Db |||||
 Qy 6269 ATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAAAAGGCGGCTTGTCTGGCGTTT 6328
 Db |||||
 Qy 2669 TTCCATAGGCTCCGCGCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGG 2728
 Db |||||
 Qy 6329 TTCCATAGGCTCCGCGCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGG 6388
 Db |||||
 Qy 2729 CGAAACCCGACAGACTATTAAGATACACAGCGTTTCCCGCTGGAAGCTCCCTCGTGGC 2788
 Db |||||
 Qy 6389 CGAAACCCGACAGACTATTAAGATACACAGCGTTTCCCGCTGGAAGCTCCCTCGTGGC 6448
 Db |||||
 Qy 2789 TCTCCTGTTCCGACCTGCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGC 2848
 Db |||||
 Qy 6449 TCTCCTGTTCCGACCTGCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGC 6508
 Db |||||
 Qy 2849 GTGGGCTTTCTCAATGCTCAGCTGTAGGTATCTCAGTTCCGCTGAGTGTAGTTCGCTCC 2908
 Db |||||
 Qy 6509 GTGGGCTTTCTCAATGCTCAGCTGTAGGTATCTCAGTTCCGCTGAGTGTAGTTCGCTCC 6568
 Db |||||
 Qy 2909 AAGCTGGGCTGTGTGACAGAACCCCGCTTCAGGCCGACCGCTGCGCTTATCCGGTAAC 2968
 Db |||||
 Qy 6569 AAGCTGGGCTGTGTGACAGAACCCCGCTTCAGGCCGACCGCTGCGCTTATCCGGTAAC 6628
 Db |||||
 Qy 2969 TATCGTCTTGAGTCCAAACCCGGTAAGACACGACTTATCGCCACTGGCAGAGCACTGGT 3028
 Db |||||
 Qy 6629 TATCGTCTTGAGTCCAAACCCGGTAAGACACGACTTATCGCCACTGGCAGAGCACTGGT 6688
 Db |||||
 Qy 3029 AACAGGATTACAGAGCCAGGTATGTAGGCGTGTACAGAGTCTTCAAGTGTGGCT 3088
 Db |||||
 Qy 6689 AACAGGATTACAGAGCCAGGTATGTAGGCGTGTACAGAGTCTTCAAGTGTGGCT 6748
 Db |||||
 Qy 3089 AACTACGGCTACACTAGAGGACAGTATTTGGTATCTCGCTCTGCTGAAAGCAAGTTACC 3148
 Db |||||
 Qy 6749 AACTACGGCTACACTAGAGGACAGTATTTGGTATCTCGCTCTGCTGAAAGCAAGTTACC 6808
 Db |||||
 Qy 3149 TTCGGAATAAGATTGGTAGTCTTTGATCCGGCAAAACAAACGACGCTGGTAGCGGTGGT 3208
 Db |||||
 Qy 6809 TTCGGAATAAGATTGGTAGTCTTTGATCCGGCAAAACAAACGACGCTGGTAGCGGTGGT 6868
 Db |||||
 Qy 3209 TTTTGTGTTGCAAGCAGAGTATACGCGCAGAAAAAGGATCTCAAGAGATCCTTTG 3268
 Db |||||
 Qy 6869 TTTTGTGTTGCAAGCAGAGTATACGCGCAGAAAAAGGATCTCAAGAGATCCTTTG 6928
 Db |||||
 Qy 3269 ATCTTTTCTACGGGCTCTGACGCTCAGTGGAAACGAAACTCAGTTAAGGGATTTGGTC 3328
 Db |||||
 Qy 6929 ATCTTTTCTACGGGCTCTGACGCTCAGTGGAAACGAAACTCAGTTAAGGGATTTGGTC 6988
 Db |||||
 Qy 3329 ATGAGGGATACATATTTGAATGATTTAGA----- 3359
 Db |||||
 Qy 6989 ATGAGATTATCAAAAGGATCTTCCACTAGATCTTTTGGGCTGGCGAAGAACTCCAGC 7048
 Db |||||
 Qy 3360 -----AAAATAACAAATAGGGTTCGCGCACATTTTCCCGCAAAAG 3401
 Db |||||
 Qy 7049 ATGAGATCCCGGCTGGAGGATCATCAGCGGGCTCCGGAACAGTTCGGAAGCCC 7108
 Db |||||
 Qy 3402 TGCCACCTGTATCGGTG-----TGAAATACCGCACAGATGCGTAAAGAGAAAT 3451
 Db |||||
 Qy 7109 AACCTTTTACAGAGCGCGGTGGAAATCGAAATCTCGTGTAGGAGGTGGGCGTCTGCT 7168
 Db |||||
 Qy 3452 ACCGATACAGAAATTTAAGGTTAATTAATTCAGAGAACCTCGTCAAGAGCCATAGA 3511
 Db |||||
 Qy 7169 TGGTGGCTCATTTCCGAACCCCAAGTCCGCTCAGAAAGAACTCGTCAAGAGCCATAGA 7228
 Db |||||
 Qy 3512 AGGCGATGCGCTCGGAATCGGAGCGCGATACCGTAAAGACACGAGGAACGCTCAGCCC 3571
 Db |||||
 Qy 7229 AGGCGATGCGCTCGGAATCGGAGCGCGATACCGTAAAGACACGAGGAACGCTCAGCCC 7288
 Db |||||

Qy 3572 ATTGCGCGCAAGCTCTTACAGCAATATCAGGGTAGCAACGCTATCTCTGATAGCGGT 3631
 Db |||||
 Qy 7289 ATTGCGCGCAAGCTCTTACAGCAATATCAGGGTAGCAACGCTATCTCTGATAGCGGT 7348
 Db |||||
 Qy 3632 CGGCCACACCCAGCGCGCACAGTCCGATGAATCAGAAAAAGCGGCCATTTTCCACCATGA 3691
 Db |||||
 Qy 7349 CGGCCACACCCAGCGCGCACAGTCCGATGAATCAGAAAAAGCGGCCATTTTCCACCATGA 7408
 Db |||||
 Qy 3692 TATTGCGCAAGCAGGCGATCGCCATGGGTACAGCAGAGATCTCTCGCGTCGGGCAATGTCG 3751
 Db |||||
 Qy 7409 TATTGCGCAAGCAGGCGATCGCCATGGGTACAGCAGAGATCTCTCGCGTCGGGCAATGTCG 7468
 Db |||||
 Qy 3752 CTTGAGCCTGGGCAACAGTTTCGGCTGGCGGAGCCCTCTGATGCTCTTTCGTCAGATCAT 3811
 Db |||||
 Qy 7469 CTTGAGCCTGGGCAACAGTTTCGGCTGGCGGAGCCCTCTGATGCTCTTTCGTCAGATCAT 7528
 Db |||||
 Qy 3812 CTTGATCGAAGACCGGCTTCCATCCGAGTACGTCGTCGTCGATCGATGTTTCGCTT 3871
 Db |||||
 Qy 7529 CTTGATCGAAGACCGGCTTCCATCCGAGTACGTCGTCGTCGATCGATGTTTCGCTT 7588
 Db |||||
 Qy 3872 GGTGGTGGGAGGAGTAGCGGATCAAGCGTATGAGCGCGGATGAGCGCGGATGAGCATGAGCCA 3931
 Db |||||
 Qy 7589 GGTGGTGGGAGGAGTAGCGGATCAAGCGTATGAGCGCGGATGAGCATGAGCCA 7648
 Db |||||
 Qy 3932 TGATGGATATCTTCTCGGAGGAGCAAGGTGAGATGACAGAGATCTCTGCGCCGCACTT 3991
 Db |||||
 Qy 7649 TGATGGATATCTTCTCGGAGGAGCAAGGTGAGATGACAGAGATCTCTGCGCCGCACTT 7708
 Db |||||
 Qy 3992 CGCCCAATAGCAGCAGTCCCTTCCGCTTCAGTGAACGCTCGAGCACAGCTGCGCAAG 4051
 Db |||||
 Qy 7709 CGCCCAATAGCAGCAGTCCCTTCCGCTTCAGTGAACGCTCGAGCACAGCTGCGCAAG 7768
 Db |||||
 Qy 4052 GAACGCGCTGTCGCGCACGATGAGCGCGCTGCTCTTTCGAGTTCATTCAGGG 4111
 Db |||||
 Qy 7769 GAACGCGCTGTCGCGCACGATGAGCGCGCTGCTCTTTCGAGTTCATTCAGGG 7828
 Db |||||
 Qy 4112 CACGCGCAGGTCTTGACAAAGAACCGGGCGCCCTCGCTGACAGCGGAAACA 4171
 Db |||||
 Qy 7829 CACGCGCAGGTCTTGACAAAGAACCGGGCGCCCTCGCTGACAGCGGAAACA 7888
 Db |||||
 Qy 4172 CGCGCGCATCAGAGCAGCGGATGCTGTCGCGCAGTATAGCCGAATAGCCTCTCCA 4231
 Db |||||
 Qy 7889 CGCGCGCATCAGAGCAGCGGATGCTGTCGCGCAGTATAGCCGAATAGCCTCTCCA 7948
 Db |||||
 Qy 4232 CCCAAGCGCGGAGAACCTCGTGCAATCATCTTGTTCATATGTCGAAACGATCTCTC 4291
 Db |||||
 Qy 7949 CCCAAGCGCGGAGAACCTCGTGCAATCATCTTGTTCATATGTCGAAACGATCTCTC 8008
 Db |||||
 Qy 4292 ATCTGCTCTTTCATCAGAGCTTGCCTCCCTGCGCCATCAG 4332
 Db |||||
 Qy 8009 ATCTGCTCTTTCATCAGATCTTTCATCCCTGCGCCATCAG 8049
 Db |||||

RESULT 2
 US-08-472-809B-8
 ; Sequence 8, Application US/08472809B
 ; Patent No. 5925564
 ; GENERAL INFORMATION:
 ; APPLICANT: Schwartz, Robert J.
 ; APPLICANT: DeMayo, Franco J.
 ; APPLICANT: O'Malley, Bert W.
 ; TITLE OF INVENTION: Expression Vector Systems and
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/98/472.809B
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,846
FILING DATE: March 9, 1994
APPLICATION NUMBER: 07/789,919
FILING DATE: No. 5925564ember 6, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 214/212
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5707 bases
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-472-809B-8

Query Match 39.7%; Score 1719; DB 2; Length 5707;
Best Local Similarity 90.8%; Pred. No. 1.2e-280;
Matches 1923; Conservative 0; Mismatches 5; Indels 191; Gaps 1;
Qy 2214 CCAGCTTTTGTTCCTTTAGTAGGGTTAAATTCGAGCTTGGGCTAATCATGTGCTATAGC 2273
Db 3477 CCAGCTTTTGTTCCTTTAGTAGGGTTAAATTCGAGCTTGGGCTAATCATGTGCTATAGC 3536
Qy 2274 TGTTCCTGTGTGAATTTGTATCCGCTCAAAATTCACACAAATACAGAGCGGAGCA 2333
Db 3537 TGTTCCTGTGTGAATTTGTATCCGCTCAAAATTCACACAAATACAGAGCGGAGCA 3596
Qy 2334 TAAAGTGAAGCTCGGGTGCCTAATGAGTAGCTAACTCACATTAATTTGCGTTCGCT 2393
Db 3597 TAAAGTGAAGCTCGGGTGCCTAATGAGTAGCTAACTCACATTAATTTGCGTTCGCT 3656
Qy 2394 CACTGCCCGCTTTCCAGTCGGGAAACCTGTGCTGCGAGCTGCATTAATGATCGGCCAAC 2453
Db 3657 CACTGCCCGCTTTCCAGTCGGGAAACCTGTGCTGCGAGCTGCATTAATGATCGGCCAAC 3716
Qy 2454 GCGCGGGAGAGCGGTTGCGTATTCGGCGCTCTTCGCTTCTCGCTCACTGACTCGC 2513
Db 3717 GCGCGGGAGAGCGGTTGCGTATTCGGCGCTCTTCGCTTCTCGCTCACTGACTCGC 3776
Qy 2514 TCGCTCGGTCTGTTTCGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAAACGCT 2573
Db 3777 TCGCTCGGTCTGTTTCGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAAACGCT 3836
Qy 2574 TATCCACAGAAATCGGGGTAACGCGAGGAAGAACATGTGAGCAAAAGGCGCAGAAAGG 2633
Db 3837 TATCCACAGAAATCAGGGGTAACGCGAGGAAGAACATGTGAGCAAAAGGCGCAGAAAGG 3896
Qy 2634 CCAGGACCGTAAAGAGCGCGTTCGCTGCGCTTTTCCATAGCTCCGCCCCCTGACG 2693
Db 3897 CCAGGACCGTAAAGAGCGCGTTCGCTGCGCTTTTCCATAGCTCCGCCCCCTGACG 3956
Qy 2694 AGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGAT 2753
Db 3957 AGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGAT 4016
Qy 2754 ACCAGGGCTTCCCTCGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCTCGCGCTTA 2813
Db 4017 ACCAGGGCTTCCCTCGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCTCGCGCTTA 4076

Qy 2814 CCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCAATGCTCAGCT 2873
Db 4077 CCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCAATGCTCAGCT 4136
Qy 2874 GTAGGTATCTCAGTTCCGTTAGGTGCTTCGCTCCAAAGCTGGGCTGTGTGCAAGAACCC 2933
Db 4137 GTAGGTATCTCAGTTCCGTTAGGTGCTTCGCTCCAAAGCTGGGCTGTGTGCAAGAACCC 4196
Qy 2934 CCGTTACGCCCCGAGCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCAACCCGGTAA 2993
Db 4197 CCGTTACGCCCCGAGCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCAACCCGGTAA 4256
Qy 2994 GACACGACTTATCGCACTGGCAGCAGCACTGTAACAGATTTAGCAGAGCAGGATG 3053
Db 4257 GACACGACTTATCGCACTGGCAGCAGCACTGTAACAGATTTAGCAGAGCAGGATG 4316
Qy 3054 TAGCGGTGCTACAGAGTTCTTGAAGTGTGGCTAACTACGCTACACTAGAGAGCAG 3113
Db 4317 TAGCGGTGCTACAGAGTTCTTGAAGTGTGGCTAACTACGCTACACTAGAGAGCAG 4376
Qy 3114 TATTTGCTATCTGCGCTCTGCTGAGCAGTACCTTCGAAAAAGAGTTGGTAGCTCTT 3173
Db 4377 TATTTGCTATCTGCGCTCTGCTGAGCAGTACCTTCGAAAAAGAGTTGGTAGCTCTT 4436
Qy 3174 GATCCGCAAAACAAACACCGCTGTGAGCGTGTGTTTTTTTGTTCGCAACGAGCAGATTA 3233
Db 4437 GATCCGCAAAACAAACACCGCTGTGAGCGTGTGTTTTTTTGTTCGCAACGAGCAGATTA 4496
Qy 3234 CCGCAGAAAAAAGAGTCTCAAGAAAGTCTTTTGTGATCTTTTCTACGGGCTTGACGCTC 3293
Db 4497 CCGCAGAAAAAAGAGTCTCAAGAAAGTCTTTTGTGATCTTTTCTACGGGCTTGACGCTC 4554
Qy 3294 AGTGGAAACGAAACTCACGTTAAGGGATTTTGTGCTATGAGCGGATACATATTTGAATGTA 3353
Db 4555 ----- 4554
Qy 3354 TTTAGAAAAATAAAATAAGGGTTTCGCGCACATTTTCCCGAAAGTGCCACTGTAT 3413
Db 4555 ----- 4554
Qy 3414 GCGGTGTGAATAACCGCACAGATGCGTAAAGAGAAATAACCGCATCAGGAAATTTGTAAGC 3473
Db 4555 ----- 4554
Qy 3474 GTTAAATTAATTCAGAAACTCGTCAAGAGCGCATAGAGCGCATGCGCTCGGATCGG 3533
Db 4555 -----TCAGAAAGAACTCGTCAAGAGCGCATAGAGCGCATGCGCTCGGATCGG 4605
Qy 3534 AGCGGCGATACCGTAAAGCACGAGAGCGGTGAGCGCATTCGCGCAAGCTCTTCAGC 3593
Db 4606 AGCGGCGATACCGTAAAGCACGAGAGCGGTGAGCGCATTCGCGCAAGCTCTTCAGC 4665
Qy 3594 AATATCAGGGTAGCAACGCTATGTCTGATAGCGGTCCGCCACACCCAGCGGCCACA 3653
Db 4666 AATATCAGGGTAGCAACGCTATGTCTGATAGCGGTCCGCCACACCCAGCGGCCACA 4725
Qy 3654 GTCCATGAATCCAGAAAAAGGCGCATTTTCCACCATGATATTCGGCAGCAGGATCGCC 3713
Db 4726 GTCCATGAATCCAGAAAAAGGCGCATTTTCCACCATGATATTCGGCAGCAGGATCGCC 4785
Qy 3714 ATGGGTCAACGACGAGATCTCGCGCTGGGCGATGCTCGCTTCAGCTTCGCGCAACAGTTTC 3773
Db 4786 ATGGGTCAACGACGAGATCTCGCGCTGGGCGATGCTCGCGCTTCGCGCAACAGTTTC 4845
Qy 3774 GGCTGCGGAGCGCTGATGCTTTCTGCTCCAGATCATCTGATCGCAAGACCGGCTTC 3833
Db 4846 GGCTGCGGAGCGCTGATGCTTTCTGCTCCAGATCATCTGATCGCAAGACCGGCTTC 4905
Qy 3834 CATCCAGTACGCTCGCTCGATGCGATGTTTTTGTGCTGCTGATGCTGCGAGGATGAGC 3893
Db 4906 CATCCAGTACGCTCGCTCGATGCGATGTTTTTGTGCTGCTGATGCTGCGAGGATGAGC 4965

QY 3894 CGGATCAAGCTATGACAGCCCGCGATTCGATCAAGCAATGATGATATCTTCGCGAGG 3953
 Db CGGATCAAGCTATGACAGCCCGCGATTCGATCAAGCAATGATGATATCTTCGCGAGG 5025
 QY 3954 AGCAAGGTGAGATGACAGGAGATCCTGCCCGGCACTTCGCCCAATAGCAGCCAGTCCCT 4013
 Db AGCAAGGTGAGATGACAGGAGATCCTGCCCGGCACTTCGCCCAATAGCAGCCAGTCCCT 5085
 QY 4014 TCCCGCTTCAGTGAACAAAGTGCAGACAGCTGCAGAAAGACGCCCGCTCGTGGCCAGCCA 4073
 Db TCCCGCTTCAGTGAACAAAGTGCAGACAGCTGCAGAAAGACGCCCGCTCGTGGCCAGCCA 5145
 QY 4074 CGATAGCGCGCTGCTGCTTGGAGTTATTCAGGGCAGCAGAGTCGCTTCGAC 4133
 Db CGATAGCGCGCTGCTGCTGCTGAGTTATTCAGGGCAGCAGAGTCGCTTCGAC 5205
 QY 4134 AAAAAGAACCGGGCGCCCTCGCTGACAGCCGGAACACGCGGCATCAGAGCAGCCGAT 4193
 Db AAAAAGAACCGGGCGCCCTCGCTGACAGCCGGAACACGCGGCATCAGAGCAGCCGAT 5265
 QY 4194 TGTCTGTTGTCGCCAGTCAATAGCCGATAGCTCTCCACCAAGCGCGGAGAACCTGC 4253
 Db TGTCTGTTGTCGCCAGTCAATAGCCGATAGCTCTCCACCAAGCGCGGAGAACCTGC 5325
 QY 4254 GTGCAATCCATCTGTTCAATCATGCGAAACGATCCTCATCTGCTCTTGTATCAGAGCT 4313
 Db GTGCAATCCATCTGTTCAATCATGCGAAACGATCCTCATCTGCTCTTGTATCAGATCT 5385
 QY 4314 TGATCCCTCGCCATCAG 4332
 Db TGATCCCTCGCCATCAG 5404

RESULT 3

US-09-479-122-19
 ; Sequence 19, Application US/09479122
 ; Patent No. 6410266
 ; GENERAL INFORMATION:
 ; APPLICANT: HARRINGTON, JOHN J.
 ; APPLICANT: SHERP, BRUCE
 ; APPLICANT: RUNDLETT, STEPHEN
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
 ; TITLE OF INVENTION: ENDOGENOUS GENES
 ; FILE REFERENCE: 0221-0003C
 ; CURRENT APPLICATION NUMBER: US/09/479,122
 ; CURRENT FILING DATE: 2000-01-07
 ; PRIOR APPLICATION NUMBER: 09/276,820
 ; PRIOR FILING DATE: 1999-03-26
 ; PRIOR APPLICATION NUMBER: 09/159,643
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 08/941,223
 ; PRIOR FILING DATE: 1997-09-26
 ; PRIOR APPLICATION NUMBER: 09/263,814
 ; PRIOR FILING DATE: 1999-03-08
 ; PRIOR APPLICATION NUMBER: 09/253,022
 ; PRIOR FILING DATE: 1999-02-19
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 19
 ; LENGTH: 4644
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-479-122-19

Query Match 36.6%; Score 1586.2; DB 3; Length 4644;
 Best Local Similarity 96.0%; Pred No. 2.8e-258;
 Matches 1656; Conservative 0; Mismatches 23; Indels 46; Gaps 1;
 QY 2608 CATGTGAGCAAAAGGCCAGCAAAAGCCAGGAACCGTAAAAAGCGCGTTCGTCGCGTT 2667
 Db 1302 CATGTGAGCAAAAGGCCAGCAAAAGCCAGGAACCGTAAAAAGCGCGTTCGTCGCGTT 1361

QY 2668 TTTCCATAGGCTCGCCCCCTGACGAGCATCACAAAAATCGAGCTCAAGTCAGAGGTG 2727
 Db TTTCCATAGGCTCGCCCCCTGACGAGCATCACAAAAATCGAGCTCAAGTCAGAGGTG 1421
 QY 2728 GCAGAAACCCGACAGGACTATAAAGATACACAGGGGTTCCTCCCTGGAAGCTCCCTCGTGG 2787
 Db GCAGAAACCCGACAGGACTATAAAGATACACAGGGGTTCCTCCCTGGAAGCTCCCTCGTGG 1481
 QY 2788 CTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAAG 2847
 Db CTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAAG 1541
 QY 2848 CGTGGCGCTTCTCAATGCTCAGCTGATGATCTCAGTTCGGTGTAGGTGCTGCTC 2907
 Db CGTGGCGCTTCTCATAGCTCAGCTGATGATCTCAGTTCGGTGTAGGTGCTGCTC 1601
 QY 2908 CAAGCTGGGCTGTGTGACGAAACCCCGCTTCAGCCCGACCGCTGCGCTTATCCGGTAA 2967
 Db CAAGCTGGGCTGTGTGACGAAACCCCGCTTCAGCCCGACCGCTGCGCTTATCCGGTAA 1661
 QY 2968 CTATCGTCTTGAAGTCCAAACCCCGGTAAAGACGATTCATCGCACTGGCAGCAGCACTGG 3027
 Db CTATCGTCTTGAAGTCCAAACCCCGGTAAAGACGATTCATCGCACTGGCAGCAGCACTGG 1721
 QY 3028 TAACAGGATTAGCAGAGGAGTATGAGCGGTGCTACAGAGTCTTGAAGTGGTGGCC 3087
 Db TAACAGGATTAGCAGAGGAGTATGAGCGGTGCTACAGAGTCTTGAAGTGGTGGCC 1781
 QY 3088 TAACTACGGCTACACTAGAAGGACAGTATTTGGTGTATCTGCGCTCTGCTGAAGCAGTTAC 3147
 Db TAACTACGGCTACACTAGAAGGACAGTATTTGGTGTATCTGCGCTCTGCTGAAGCAGTTAC 1841
 QY 3148 CTTCCGAAAAGAGTGGTAGCTCTTGATTCGGGCAAAACCAACCGCTGGTAGCGGTG 3207
 Db CTTCCGAAAAGAGTGGTAGCTCTTGATTCGGGCAAAACCAACCGCTGGTAGCGGTG 1901
 QY 3208 TTTTGTGTTTGAAGCAGCAGATTTACGCGCAGAAAAAAGGATCTCAAGAGATCTCTTT 3267
 Db TTTTGTGTTTGAAGCAGCAGATTTACGCGCAGAAAAAAGGATCTCAAGAGATCTCTTT 1961
 QY 3268 GATCTTTTCTACGGGCTCTGACGCTCAGTGAAGCAAGCAAACTCAGTTAAGGATTTTGGT 3327
 Db GATCTTTTCTACGGGCTCTGACGCTCAGTGAAGCAAGCAAACTCAGTTAAGGATTTTGGT 2021
 QY 3328 CATGAGCGGATACATATTTGATGATTTTGAAGAAAAAATAAATAAGGTTCCCGGCAC 3387
 Db CATGAGATTAATCAAAAAAGGATCTTCACTAGA----- 2053
 QY 3388 ATTTCCCGAAAAGTGCACCTGTATGCGGTGTAATAATACCGCACAGATGCGTAAGGAGA 3447
 Db ATTTCCCGAAAAGTGCACCTGTATGCGGTGTAATAATACCGCACAGATGCGTAAGGAGA 2095
 QY 3448 AAATAACCGCATCAGGAAATTTGAAGCGTTAATAATTCAGAGAACTCTCAAGAGGCGA 3507
 Db AAATAACCGCATCAGGAAATTTGAAGCGTTAATAATTCAGAGAACTCTCAAGAGGCGA 2155
 QY 3508 TAGAAGCGGATGCGGTGGAATTCGGGACCGGATACCGTAAGCAGGAGGAGGCTCA 3567
 Db TAGAAGCGGATGCGGTGGAATTCGGGACCGGATACCGTAAGCAGGAGGAGGCTCA 2215
 QY 3568 GCCCATTCGCGCAAGCTCTTTCAGCAATATTCAGGGTAGCCCAAGCTATGCTCTGATAG 3627
 Db GCCCATTCGCGCAAGCTCTTTCAGCAATATTCAGGGTAGCCCAAGCTATGCTCTGATAG 2275
 QY 3628 CGGTCGCGCACACCCAGCGGCGCAGTCGATGAATTCAGAAAAAGCGGCCATTTTCCACC 3687
 Db CGGTCGCGCACACCCAGCGGCGCAGTCGATGAATTCAGAAAAAGCGGCCATTTTCCACC 2335
 QY 3688 ATGATATTCGAGCAGGAGTCCGATGGGTGACGAGGATCTCTCCCGTCGGGCGATG 3747
 Db ATGATATTCGAGCAGGAGTCCGATGGGTGACGAGGATCTCTCCCGTCGGGCGATG 2395
 QY 3748 CTCGCTTTGAGCCTGGCGAACAGGTTTCGGCTGGCGGAGCCCTGATGCTCTTCTGTCAG 3807

Db 2216 GCCCATGCGCCCAAGCTCTTACGCAATATACGGGTAGCAACGCTATGCTCTGATG 2275
Qy 3628 CGGTCCGCGCACACCCAGCGCCACAGTCAGTGAATCCAGAAAGCGGCATTTTCCACC 3687
Db 2276 CGGTCCGCGCACACCCAGCGCCACAGTCAGTGAATCCAGAAAGCGGCATTTTCCACC 2335
Qy 3688 ATGATATTGGCAAGCAGGCGATCGCCATGGGTGTCAGCAGAGATCCTCGCGTCGGGCGATG 3747
Db 2336 ATGATATTGGCAAGCAGGCGATCGCCATGGGTGTCAGCAGAGATCCTCGCGTCGGGCGATG 2395
Qy 3748 CTCGCCCTGAGCTGGCGGAACAGTTCCGCTGGCGGAGCCCTGATGCTCTTGTGTCAGA 3807
Db 2396 CTCGCCCTGAGCTGGCGGAACAGTTCCGCTGGCGGAGCCCTGATGCTCTTGTGTCAGA 2455
Qy 3808 TCATCTCTGATCGCAAGACCGGCTTCATCCGAGTACGTGCTGCTCGATCGAGCTGTTTC 3867
Db 2456 TCATCTCTGATCGCAAGACCGGCTTCATCCGAGTACGTGCTGCTCGATCGAGCTGTTTC 2515
Qy 3868 GCTTGGTGTGATGAGTGGGCGAGGTAGCGCGGATCAAGCGTATGACGCGCGCGCATTTGCAATCA 3927
Db 2516 GCTTGGTGTGATGAGTGGGCGAGGTAGCGCGGATCAAGCGTATGACGCGCGCGCATTTGCAATCA 2575
Qy 3928 GCCATGATGATATCTTCTCGGCAAGGAGCAAGGTGAGATGACAGGAGATCCTGCGCCGCG 3987
Db 2576 GCCATGATGATATCTTCTCGGCAAGGAGCAAGGTGAGATGACAGGAGATCCTGCGCCGCG 2635
Qy 3988 ACTTCGCCCAATAGCAGCGAGTCCCTTCCCGCTTCAGTGACACGTCGAGCAGACGTCGG 4047
Db 2636 ACTTCGCCCAATAGCAGCGAGTCCCTTCCCGCTTCAGTGACACGTCGAGCAGACGTCGG 2695
Qy 4048 CAAGGAACGCGCTGCTGGCGCAGCCAGATAGCGCGCTGCTGCTCTTGCAGTTCAATTC 4107
Db 2696 CAAGGAACGCGCTGCTGGCGCAGCCAGATAGCGCGCTGCTGCTCTTGCAGTTCAATTC 2755
Qy 4108 AGGCAACGCGACAGGTGCTTGAACAAAGAACCGGGCGCCCTGCGCTGACAGCGCG 4167
Db 2756 AGGCAACGCGACAGGTGCTTGAACAAAGAACCGGGCGCCCTGCGCTGACAGCGCG 2815
Qy 4168 AACACGCGCGCATCAGACGACGCGATTTGCTGTTGTCGCCAGTCATAGCCGAATAGCCTC 4227
Db 2816 AACACGCGCGCATCAGACGACGCGATTTGCTGTTGTCGCCAGTCATAGCCGAATAGCCTC 2875
Qy 4228 TCCACCAAGCGCGCGAGAACCTGCGTGCATCCATCTTTGTTCAATCATCGCAAGCAT 4287
Db 2876 TCCACCAAGCGCGCGAGAACCTGCGTGCATCCATCTTTGTTCAATCATCGCAAGCAT 2935
Qy 4288 CCTCATCTCTCTTGTATCAGAGCTTGATCCCTGCGCCATCAG 4332
Db 2936 CCTCATCTCTCTTGTATCAGAGCTTGATCCCTGCGCCATCAG 2980

RESULT 6
US-09-481-282-19
; Sequence 19, Application US/09481282
; Patent No. 6541221
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003US
; CURRENT APPLICATION NUMBER: US/09/481,282
; CURRENT FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19

; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1.1
; SEQ ID NO 19
; LENGTH: 4644
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-481-282-19

Query Match 36.6%; Score 1586.2; DB 3; Length 4644;
Best Local Similarity 96.0%; Pred. No. 2.8e-258;
Matches 1656; Conservative 0; Mismatches 23; Indels 46; Gaps 1;

Qy 2608 CATGTGAGCAAAAGGCCAGCAAAAGGCCAGAAACCGTAAAGAGCCGCGTGTGCTGCGGTT 2667
Db 1302 CATGTGAGCAAAAGGCCAGCAAAAGGCCAGAAACCGTAAAGAGCCGCGTGTGCTGCGGTT 1361
Qy 2668 TTTTCCATAGGCTCCGCCCTCCGCTGACGAGCATCAAAAATCGAGGCTCAAGTCAGAGGTG 2727
Db 1362 TTTTCCATAGGCTCCGCCCTCCGCTGACGAGCATCAAAAATCGAGGCTCAAGTCAGAGGTG 1421
Qy 2728 GCGAAACCCGACAGGACTATAAAGATACACAGGCGTTTCCCTTGGAAAGCTCCCTCGTGG 2787
Db 1422 GCGAAACCCGACAGGACTATAAAGATACACAGGCGTTTCCCTTGGAAAGCTCCCTCGTGG 1481
Qy 2788 CTCTCTGTTCGACCCCTGCGCTTACCGGATACCTGTCCGCGCTTCTCCCTTCGCGAAG 2847
Db 1482 CTCTCTGTTCGACCCCTGCGCTTACCGGATACCTGTCCGCGCTTCTCCCTTCGCGAAG 1541
Qy 2848 CGTGGCGCTTCTCAATGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGTGTGCTGCTC 2907
Db 1542 CGTGGCGCTTCTCATAAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGTGTGCTGCTC 1601
Qy 2908 CAAGCTGGGCTGTGTCAGCAACCCCGTTACAGCCCGCTGCGCGCTTATCCCGGTAA 2967
Db 1602 CAAGCTGGGCTGTGTCAGCAACCCCGTTACAGCCCGCTGCGCGCTTATCCCGGTAA 1661
Qy 2968 CTATCTGTTCAGTCAACCCCGTTAAAGACAGCTTATTCGCCACTGACAGCAGCACTGG 3027
Db 1662 CTATCTGTTCAGTCAACCCCGTTAAAGACAGCTTATTCGCCACTGACAGCAGCACTGG 1721
Qy 3028 TAACAGGTTAGCAGAGCGAGGTATGAGCGGTGTCTACAGAGTTCTTGAAGTGTGGCC 3087
Db 1722 TAACAGGTTAGCAGAGCGAGGTATGAGCGGTGTCTACAGAGTTCTTGAAGTGTGGCC 1781
Qy 3088 TAATACGCGTACACTAGAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTAC 3147
Db 1782 TAATACGCGTACACTAGAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTAC 1841
Qy 3148 CTTTCGAAAAAGAGTTGGTAGCTCTTTGATCCGCGCAAAACAAACCAACCGCTGTTAGCGGTG 3207
Db 1842 CTTTCGAAAAAGAGTTGGTAGCTCTTTGATCCGCGCAAAACAAACCAACCGCTGTTAGCGGTG 1901
Qy 3208 TTTTGTGTTCGAAAGCAGAGTTACCGCGCAAAAAAAGGATCTCAGAAAGATCTTTT 3267
Db 1902 TTTTGTGTTCGAAAGCAGAGTTACCGCGCAAAAAAAGGATCTCAGAAAGATCTTTT 1961
Qy 3268 GATCTTTTCTACGGGCTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGATTTTGGT 3327
Db 1962 GATCTTTTCTACGGGCTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGATTTTGGT 2021
Qy 3328 CATGACGGGATACATATTTGAATGTATTTAGAAAAATAAATAATAGGGGTTCCGCGCAC 3387
Db 2022 CATGAGATTTATCAAAAAGGATCTTACCTAGA----- 2053
Qy 3388 ATTTCCCGGAAAGTCCCACTGTATGCGGTGTGAATATCCGCACAGATCGCTAAGAGA 3447
Db 2054 -----TCCCTTTTATCGGTGTGAATATCCGCACAGATCGCTAAGAGA 2095
Qy 3448 AAATACCGCATCAGGAAATTTGAAGCGTTAATAATTTAGAAAGAACTCGTCAAGAAAGCGGA 3507
Db 2096 AAATACCGCATCAGGAAATTTGAAGCGTTAATAATTTAGAAAGAACTCGTCAAGAAAGCGGA 2155
Qy 3508 TAGAAGCGGATGCGCTGCGAATTCGGAGCGCGGCGATACCGTAAAGACGAGGAAGCGGTCA 3567

Db 2156 TAGAAGTCGATGCGCTGCGAATCGGAGCGCGGATACCGTAAGACAGGAGCGGTCA 2215
Qy 3568 GCCCATTCGCGCGCAAGCTCTTCAGCAATATACAGGGTAGCGCAAGCTATGCTCTGATAG 3627
Db 2216 GCCCATTCGCGCGCAAGCTCTTCAGCAATATACAGGGTAGCGCAAGCTATGCTCTGATAG 2275
Qy 3628 CCGTCCGCGCACACCCAGCGCGGCCACAGTCGATGAATCCAGAAAAAGCGGCCATTTTCCACC 3687
Db 2276 CCGTCCGCGCACACCCAGCGCGGCCACAGTCGATGAATCCAGAAAAAGCGGCCATTTTCCACC 2335
Qy 3688 ATGATATTTCGCGAGCAGGAGCATTCGCCATGCGGTGACGAGCATCTGCGCGTGGGATG 3747
Db 2336 ATGATATTTCGCGAGCAGGAGCATTCGCCATGCGGTGACGAGCATCTGCGCGTGGGATG 2395
Qy 3748 CTCGCTTGAGCTGCGGCAACAGTTTCGCTCGCGAGCCCTGATGCTCTTCGTCAGAGA 3807
Db 2396 CTCGCTTGAGCTGCGGCAACAGTTTCGCTCGCGAGCCCTGATGCTCTTCGTCAGAGA 2455
Qy 3808 TCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGATCGCATGTTTC 3867
Db 2456 TCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGATCGCATGTTTC 2515
Qy 3868 GCTTGGTGGTGCATGGGAGGATAGCCGGATCAAGCGTATGAGCCGCGCATTTGCATCA 3927
Db 2516 GCTTGGTGGTGCATGGGAGGATAGCCGGATCAAGCGTATGAGCCGCGCATTTGCATCA 2575
Qy 3928 GCCATGATGGATCTTCTCGCGAGGACAGGTGAGATGACAGGAGATCTGCCCCGGC 3987
Db 2576 GCCATGATGGATCTTCTCGCGAGGACAGGTGAGATGACAGGAGATCTGCCCCGGC 2635
Qy 3988 ACTTCGCCCAATAGCAGCGAGTCCCTTCCCGCTTCAGTGACAAAGTCGAGCACAGCTCG 4047
Db 2636 ACTTCGCCCAATAGCAGCGAGTCCCTTCCCGCTTCAGTGACAAAGTCGAGCACAGCTCG 2695
Qy 4048 CAAAGAAACGCGCTGTCGCGAGCCACGATAGCCGCTGCTCTGCTGAGTTTCATTC 4107
Db 2696 CAAAGAAACGCGCTGTCGCGAGCCACGATAGCCGCTGCTCTGCTGAGTTTCATTC 2755
Qy 4108 AGGCGCACCGGACAGTTCGCTTTGACAAAAGAACCGCGCGCTGCGCTGACAGCGG 4167
Db 2756 AGGCGCACCGGACAGTTCGCTTTGACAAAAGAACCGCGCGCTGCGCTGACAGCGG 2815
Qy 4168 AACACGGCGGCATCAGACAGCGCATGCTGTTGTCGCGAGTCATAGCCGAATAGCTC 4227
Db 2816 AACACGGCGGCATCAGACAGCGCATGCTGTTGTCGCGAGTCATAGCCGAATAGCTC 2875
Qy 4228 TCACCCCAAGCGCGGAGAACCTGCGTCAATCCATCTGTTCAATCATCGGAACGAT 4287
Db 2876 TCACCCCAAGCGCGGAGAACCTGCGTCAATCCATCTGTTCAATCATCGGAACGAT 2935
Qy 4288 CCTCATCTGCTCTTTGATCAGAGCTTGATCCCGCTGCGGCATCAG 4332
Db 2936 CCTCATCTGCTCTTTGATCAGAGCTTGATCCCGCTGCGGCATCAG 2980

RESULT 7
US-09-455-659A-19
; Sequence 19, Application US/09455659A
; Patent No. 6602686
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; ENDGENOUS GENES
; FILE REFERENCE: 0221-0003A
; CURRENT APPLICATION NUMBER: US/09/455,659A
; CURRENT FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08

; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 4644
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-455-659A-19

Query Match 36.6%; Score 1586.2; DB 3; Length 4644;
Best Local Similarity 96.0%; Pred. No. 2.8e-258;
Matches 1656; Conservative 0; Mismatches 23; Indels 46; Gaps 1;
Qy 2608 CATGTGAGCAAAAGGCGCAGCAAAAGGCGCAGCAAAAGGCGGTAAGAAAGGCGGTTGCTGGCGTT 2667
Db 1302 CATGTGAGCAAAAGGCGCAGCAAAAGGCGCAGCAAAAGGCGGTTGCTGGCGTT 1361
Qy 2668 TTTCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGTG 2727
Db 1362 TTTCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGTG 1421
Qy 2728 GCGAAACCCGACAGGACTATAAAGATACCAAGCGGCTTTCCCGCTCGGAAGCTCCCTCGTGG 2787
Db 1422 GCGAAACCCGACAGGACTATAAAGATACCAAGCGGCTTTCCCGCTCGGAAGCTCCCTCGTGG 1481
Qy 2788 CTCTCTGTTCCGACCGCTGCGCTTACCGGATACCTGTCGCGCTTCTCCCTCGGGAAG 2847
Db 1482 CTCTCTGTTCCGACCGCTGCGCTTACCGGATACCTGTCGCGCTTCTCCCTCGGGAAG 1541
Qy 2848 CGTGGCGCTTCTCAATGCTCACTGATGATCTCAGTTGCTGAGTGTAGTGTGCTGCTC 2907
Db 1542 CGTGGCGCTTCTCACTGATCACTGATGATCTCAGTTGCTGAGTGTAGTGTGCTGCTC 1601
Qy 2908 CAAGCTGGGCTGTGTGACAGAAACCCCGCTTACGCGCGACCGCTGCGCTTATCCGCTAA 2967
Db 1602 CAAGCTGGGCTGTGTGACAGAAACCCCGCTTACGCGCGACCGCTGCGCTTATCCGCTAA 1661
Qy 2968 CTATGCTTTCAGTCCAAACCCGCTAAGACACGCTTATGCGCACTGCGCAGCAGCACCTGG 3027
Db 1662 CTATGCTTTCAGTCCAAACCCGCTAAGACACGCTTATGCGCACTGCGCAGCAGCACCTGG 1721
Qy 3028 TAACAGGATTAGCAGAGCGAGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGTGGCC 3087
Db 1722 TAACAGGATTAGCAGAGCGAGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGTGGCC 1781
Qy 3088 TAACTACGGCTACACTAGAGCAGATTTGGTATCTGCGCTCTGCTGAGCCAGTTAC 3147
Db 1782 TAACTACGGCTACACTAGAGCAGATTTGGTATCTGCGCTCTGCTGAGCCAGTTAC 1841
Qy 3148 CTTCCGAAAAAGAGTTGGTGTAGTCTTTGATCCGCAACAAACCCAGCTGCTAGCGGTGG 3207
Db 1842 CTTCCGAAAAAGAGTTGGTGTAGTCTTTGATCCGCAACAAACCCAGCTGCTAGCGGTGG 1901
Qy 3208 TTTTCTTTGTTTGCAGACGAGATTAACGCGAAAAAAGGATCTCAAGAAAGATCTTTT 3267
Db 1902 TTTTCTTTGTTTGCAGACGAGATTAACGCGAAAAAAGGATCTCAAGAAAGATCTTTT 1961
Qy 3268 GATCTTTTCTACGGGCTCTGAGCTCAGTGGNACGAAACTCACGTTAAGGATTTTGGT 3327
Db 1962 GATCTTTTCTACGGGCTCTGAGCTCAGTGGNACGAAACTCACGTTAAGGATTTTGGT 2021
Qy 3328 CATGAGCGGATACATATTTGAATGATTTTAGAAAAATAAAATAAGGGGTTCCCGCGCAC 3387
Db 2022 CATGAGATTAACAAAGGATCTTCACTAGA----- 2053
Qy 3388 ATTTCCCGAAAAAGTGCCACCTGTATGCGGTGTGAAATACCCGACAGATGCGTAAGGAGA 3447
Db 2054 -----TCCCTTTTATCGGTGTGAAATACCCGACAGATGCGTAAGGAGA 2095

```

QY 3448 AAATACCCCATCAGGAATTTGAAGCGTTAAATAATTCAGAGAATCTGTCAAGAAGCGA 3507
Db 2096 AAATACCCCATCAGGAATTTGAAGCGTTAAATAATTCAGAGAATCTGTCAAGAAGCGA 2155
QY 3508 TAGAAGCGGATCGCTCGGAATTCGGAGCGCGATACCGTAAAGCAAGAGGAGCGGTCA 3567
Db 2156 TAGAAGCGGATCGCTCGGAATTCGGAGCGCGATACCGTAAAGCAAGAGGAGCGGTCA 2215
QY 3568 GCCATTCGCCGCCAAGCTCTTCAGCAATATACGGGTAGCAACGCTATGCTCTGTATAG 3627
Db 2216 GCCATTCGCCGCCAAGCTCTTCAGCAATATACGGGTAGCAACGCTATGCTCTGTATAG 2275
QY 3628 CGGTCCGCGCACACCCAGCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACC 3687
Db 2276 CGGTCCGCGCACACCCAGCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACC 2335
QY 3688 ATGATATTCGACAGCGGATCGCCATGCGGTGACGAGAGATCTCGCGTCCGGCATG 3747
Db 2336 ATGATATTCGACAGCGGATCGCCATGCGGTGACGAGAGATCTCGCGTCCGGCATG 2395
QY 3748 CTCGCCCTTACCTCGCGGAAACAGTTCCGCTGCGCGAGCCCTGATGCTCTTCGTCGAGA 3807
Db 2396 CTCGCCCTTACCTCGCGGAAACAGTTCCGCTGCGCGAGCCCTGATGCTCTTCGTCGAGA 2455
QY 3808 TCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTCTCGCTCGATCGATGTTTC 3867
Db 2456 TCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTCTCGCTCGATCGATGTTTC 2515
QY 3868 GCTTGGTGGTGAATGGCAGGTAGCCGATCAAGCGTATGACGCGCCGCGGATTCATCA 3927
Db 2516 GCTTGGTGGTGAATGGCAGGTAGCCGATCAAGCGTATGACGCGCCGCGGATTCATCA 2575
QY 3928 GCCATGATGATATCTTCTCGGAGGAGCAAGTGGATGACAGAGATCTCGCCCGGC 3987
Db 2576 GCCATGATGATATCTTCTCGGAGGAGCAAGTGGATGACAGAGATCTCGCCCGGC 2635
QY 3988 ACTTCGCCCAATAGCAGCAGTCCCTTCCGCTTCAGTGACAAGCTCGAGCAGAGTGGC 4047
Db 2636 ACTTCGCCCAATAGCAGCAGTCCCTTCCGCTTCAGTGACAAGCTCGAGCAGAGTGGC 2695
QY 4048 CAAGGAACGCCGCTGCGGAGCAGCAGATAGCCGCTGCTGCTTCGAGTTCATTC 4107
Db 2696 CAAGGAACGCCGCTGCGGAGCAGCAGATAGCCGCTGCTGCTTCGAGTTCATTC 2755
QY 4108 AGGCAACCGGACAGTCTGCTTCAAAAAGAACCGGCGCCCTCGCTGACAGCGG 4167
Db 2756 AGGCAACCGGACAGTCTGCTTCAAAAAGAACCGGCGCCCTCGCTGACAGCGG 2815
QY 4168 AACACGGCGGATCAGAGCAGCGGATGCTGTTGTGCCAGTCAATAGCCGAATAGCCTC 4227
Db 2816 AACACGGCGGATCAGAGCAGCGGATGCTGTTGTGCCAGTCAATAGCCGAATAGCCTC 2875
QY 4228 TCCACCAAGCGCGGAGAACCTGCGTCAATCATCTTGTTCATCATCGCGAAGAT 4287
Db 2876 TCCACCAAGCGCGGAGAACCTGCGTCAATCATCTTGTTCATCATCGCGAAGAT 2935
QY 4288 CCTCATCTGCTCTTCATCAGAGCTTGATCCCTCGCGCATCAG 4332
Db 2936 CCTCATCTGCTCTTCATCAGAGCTTGATCCCTCGCGCATCAG 2980

```

RESULT 8

```

US-09-484-996-19
; Sequence 19, Application US/09484996
; Patent No. 6623958
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; ENDGENOUS GENES
; FILE REFERENCE: 0221-0003H

```

```

; CURRENT APPLICATION NUMBER: US/09/484,996
; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1998-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 4644
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-484-996-19

Query Match      36.6%; Score 1586.2; DB 3; Length 4644;
Best Local Similarity 96.0%; Pred. No. 2.8e-258;
Matches 1656; Conservative 0; Mismatches 23; Indels 46; Gaps 1;

QY 2608 CATGTGAGCAAAAGGCCAGCAAAAGGCCAGAAACCGTAAAGGCGCGGTTGCTGGCGTT 2667
Db 1302 CATGTGAGCAAAAGGCCAGCAAAAGGCCAGAAACCGTAAAGGCGCGGTTGCTGGCGTT 1361
QY 2668 TTTCCATAGGCTCCGCCGCCCTGACGAGCATCAAAAATCGAGCTCAAGTCAGAGGTG 2727
Db 1362 TTTCCATAGGCTCCGCCGCCCTGACGAGCATCAAAAATCGAGCTCAAGTCAGAGGTG 1421
QY 2728 GCGAAACCCGACAGGACTATAAAGATACCAAGGCGTTTCCGCCCTGGAAGCTCCCTCGTGGC 2787
Db 1422 GCGAAACCCGACAGGACTATAAAGATACCAAGGCGTTTCCGCCCTGGAAGCTCCCTCGTGGC 1481
QY 2788 CTCCTCTGTTCCGACCCCTGCTTACCGGATACCTGTCCGCCCTTCTCCCTTCGGGAAG 2847
Db 1482 CTCCTCTGTTCCGACCCCTGCTTACCGGATACCTGTCCGCCCTTCTCCCTTCGGGAAG 1541
QY 2848 CGTGGCGCTTCTCAATGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGTTCGTTCCGCTC 2907
Db 1542 CGTGGCGCTTCTCAATGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGTTCGTTCCGCTC 1601
QY 2908 CAAGCTGGGCTGTGTGCAGAACCCCGCTTACGCGCGACCGCTGCGCCCTTATCCGGTAA 2967
Db 1602 CAAGCTGGGCTGTGTGCAGAACCCCGCTTACGCGCGACCGCTGCGCCCTTATCCGGTAA 1661
QY 2968 CTAATCGTCTTGTAGTCCAAACCCGGTAAAGACACGACTTATCGCCACTGCGCAGCAGCACTGG 3027
Db 1662 CTAATCGTCTTGTAGTCCAAACCCGGTAAAGACACGACTTATCGCCACTGCGCAGCAGCACTGG 1721
QY 3028 TAACAGGTTAGCAGAGCGAGGTATGTAGCGGCTGTACAGAGTCTTGAAGTGGTGGCC 3087
Db 1722 TAACAGGTTAGCAGAGCGAGGTATGTAGCGGCTGTACAGAGTCTTGAAGTGGTGGCC 1781
QY 3088 TAACACTCGGCTACACTAGAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTAC 3147
Db 1782 TAACACTCGGCTACACTAGAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTAC 1841
QY 3148 CTTTCGAAAAGAGTTGGTAGTCTTGTATCCGCGCAAAACAAACACCGCTGGTAGCGGTGG 3207
Db 1842 CTTTCGAAAAGAGTTGGTAGTCTTGTATCCGCGCAAAACAAACACCGCTGGTAGCGGTGG 1901
QY 3208 TTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAGAGATCTCAGAAAGATCCTTT 3267
Db 1902 TTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAGAGATCTCAGAAAGATCCTTT 1961
QY 3268 GATCTTTTCTACGGGCTCTGACGCTCAGTGGAAACGAAAACCTACGTTTAAGGGATTTTGGT 3327
Db 1962 GATCTTTTCTACGGGCTCTGACGCTCAGTGGAAACGAAAACCTACGTTTAAGGGATTTTGGT 2021
QY 3328 CATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAATAAATAGGGGTTCCGCGCAC 3387

```

```
Db 2022 CATGAGATTATCAAAAGGATCTTCACTAGA----- 2053
Qy 3388 ATTTCCCGAAAGTGCACCTGTATCGGTGTGAATACCGACACAGATCGTAAAGAGA 3447
Db 2054 -----TCTTTTATCGGTGTGAATACCGACACAGATCGTAAAGAGA 2095
Qy 3448 AAATACCGCATCAGAAATGTAAAGCGTTAATAATTCAGAAACTCGTCAAGAGCGGA 3507
Db 2096 AAATACCGCATCAGAAATGTAAAGCGTTAATAATTCAGAAACTCGTCAAGAGCGGA 2155
Qy 3508 TAGAAGCGATGCGCTGCGAATCGGAGCGCGGATACCGTAAAGACAGAGACGGTCA 3567
Db 2156 TAGAAGCGATGCGCTGCGAATCGGAGCGCGGATACCGTAAAGACAGAGACGGTCA 2215
Qy 3568 GCCCATTCGCGCGCAAGCTTTCAGCAATATCACGGGTAGCCACGCTATGCTCTGATAG 3627
Db 2216 GCCCATTCGCGCGCAAGCTTTCAGCAATATCACGGGTAGCCACGCTATGCTCTGATAG 2275
Qy 3628 CGGTCCGCCACACCCAGCGCGCCACAGTCGATGAATCCAGAAAGCGGCCATTTTCCACC 3687
Db 2276 CGGTCCGCCACACCCAGCGCGCCACAGTCGATGAATCCAGAAAGCGGCCATTTTCCACC 2335
Qy 3688 ATGATATTGGCAAGCAGAGCATTCGCCATGGGTACAGACAGATCCTCGCGTCGGGATG 3747
Db 2336 ATGATATTGGCAAGCAGAGCATTCGCCATGGGTACAGACAGATCCTCGCGTCGGGATG 2395
Qy 3748 CTGCGCTTGGCTGGCGAAACAGTTCGGCTGGCGAGCCCTGATGCTCTTCGTCCAGA 3807
Db 2396 CTGCGCTTGGCTGGCGAAACAGTTCGGCTGGCGAGCCCTGATGCTCTTCGTCCAGA 2455
Qy 3808 TCATCTCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTT 3867
Db 2456 TCATCTCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTT 2515
Qy 3868 GCTTGGTGGTCCAAATGGGAGGTAGCCGGATCAAGCGTATGAGCCGCGCATTCGATCA 3927
Db 2516 GCTTGGTGGTCCAAATGGGAGGTAGCCGGATCAAGCGTATGAGCCGCGCATTCGATCA 2575
Qy 3928 GCCATGATGATCTTTCGCGAGGACAGGTGAGATGACAGAGATCCTGCCCGGC 3987
Db 2576 GCCATGATGATCTTTCGCGAGGACAGGTGAGATGACAGAGATCCTGCCCGGC 2635
Qy 3988 ACTTCCGCCAATAGCAGCAGTCCCTTCCCGTTCCAGTGACAACTCGAGCACAGCTCG 4047
Db 2636 ACTTCCGCCAATAGCAGCAGTCCCTTCCCGTTCCAGTGACAACTCGAGCACAGCTCG 2695
Qy 4048 CAAGAAACGCGCTCGTGGCAGCAGATAGCCGCTGCTCGTCTGCGATTCATTC 4107
Db 2696 CAAGAAACGCGCTCGTGGCAGCAGATAGCCGCTGCTCGTCTGCGATTCATTC 2755
Qy 4108 AGGCGACCGGACAGTCTTGACAAAGAACCGGCGCCCTCGCTGACAGCCGG 4167
Db 2756 AGGCGACCGGACAGTCTTGACAAAGAACCGGCGCCCTCGCTGACAGCCGG 2815
Qy 4168 AACACGCGGCGCATCAGAGCAGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4227
Db 2816 AACACGCGGCGCATCAGAGCAGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2875
Qy 4228 TCACCCAAAGCGCGGAGAACTGCGTGCATTCATCTGTTGTTGTTGTTGTTGTTGTTGTTGTT 4287
Db 2876 TCACCCAAAGCGCGGAGAACTGCGTGCATTCATCTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2935
Qy 4288 CCTCATCTGCTCTTGTATCAGAGCTTGATCCCTGCGCATCAG 4332
Db 2936 CCTCATCTGCTCTTGTATCAGAGCTTGATCCCTGCGCATCAG 2980
```

RESULT 9

US-09-479-123-19

; Sequence 19, Application US/09479123

; Patent No. 6670185

; GENERAL INFORMATION:

```
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003B
; CURRENT APPLICATION NUMBER: US/09/479,123
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 4644
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-479-123-19
```

```
Query Match 36.6%; Score 1586.2; DB 3; Length 4644;
Best Local Similarity 96.0%; Pred. No. 2.8e-258;
Matches 1656; Conservative 0; Mismatches 23; Indels 46; Gaps 1;

Qy 2608 CATCTGAGCAAAAGCGCAGCAAAAGGCGCAGCAACCGTAAAGGCGCGTGTGCGGT 2667
Db 1302 CATCTGAGCAAAAGCGCAGCAAAAGGCGCAGCAACCGTAAAGGCGCGTGTGCGGT 1361
Qy 2668 TTTCATAGGCTCGCGCCCTGACGAGCATCAAAAATCGACGTCAAGTCAGAGTG 2727
Db 1362 TTTCATAGGCTCGCGCCCTGACGAGCATCAAAAATCGACGTCAAGTCAGAGTG 1421
Qy 2728 GCGAAACCGGACAGCACTATAAGATACCAAGCGTTCCTCCCTGGAAGCTCCCTCGTGC 2787
Db 1422 GCGAAACCGGACAGCACTATAAGATACCAAGCGTTCCTCCCTGGAAGCTCCCTCGTGC 1481
Qy 2788 CTCTCTGTTCCGACCTCGCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAG 2847
Db 1482 CTCTCTGTTCCGACCTCGCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAG 1541
Qy 2848 CGTGGCGTTTCTCAATGCTCAAGCTGAGTATCTAGTTCGGTGTAGTGTGCTC 2907
Db 1542 CGTGGCGTTTCTCATAGCTCAAGCTGAGTATCTAGTTCGGTGTAGTGTGCTC 1601
Qy 2908 CAAGCTGGGCTGTGTGACGAAACCCCGTTACCGCGACCGCTGCGCTTATCCGGTAA 2967
Db 1602 CAAGCTGGGCTGTGTGACGAAACCCCGTTACCGCGACCGCTGCGCTTATCCGGTAA 1661
Qy 2968 CTATCGTCTTGAGTCCAAACCGGTAAAGACAGACTTATCGCCACTGGCAGCAGCACTGG 3027
Db 1662 CTATCGTCTTGAGTCCAAACCGGTAAAGACAGACTTATCGCCACTGGCAGCAGCACTGG 1721
Qy 3028 TAACAGGATTAGCAGAGCAGGATGTAGGCGGTGCTACAGATTTCTTGAAGTGTGGCC 3087
Db 1722 TAACAGGATTAGCAGAGCAGGATGTAGGCGGTGCTACAGATTTCTTGAAGTGTGGCC 1781
Qy 3088 TAACCTACGGCTACACTAGAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTAC 3147
Db 1782 TAACCTACGGCTACACTAGAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTAC 1841
Qy 3148 CTTCCGAAAAAGAGTTGGTAGCTCTTTGATCCGCGCAAAACCAACCGCTGTAGCGGTGG 3207
Db 1842 CTTCCGAAAAAGAGTTGGTAGCTCTTTGATCCGCGCAAAACCAACCGCTGTAGCGGTGG 1901
Qy 3208 TTTTCTTTGTTGCAAGCAGCAGATTAACGCGCAAAAAAGAGATCTCAAGAGATCTTTT 3267
Db 1902 TTTTCTTTGTTGCAAGCAGCAGATTAACGCGCAAAAAAGAGATCTCAAGAGATCTTTT 1961
Qy 3268 GATCTTTCTACGGGCTCTGACGCTCAGTGGAAACGAAAACTCACGTTAAGGATTTTGT 3327
```



```
Db 1962 GATCTTTTCTACGGGGTCTGACGCTCAGTCGAAACGAACTCAGTTAAAGGATTTTGGT 2021
Qy 3328 CATGAGCGGATACATATTTGAATGATTTAGAAAATAAACAATAGGGTTCGGCGAC 3387
Db 2022 CATGAGATTACAAAAGGATCTTCACTTGA----- 2053
Qy 3388 ATTTCCCGGAAAGTGCACCTGTATGCGGTGTGAAATACCGCACAGATCGTAAAGGAGA 3447
Db 2054 -----TCCTTTTATCGGTGTGAATACCGCACAGATCGTAAAGGAGA 2095
Qy 3448 AAATACCGCATCAGAAATTTGTAAGCGTTAATAATTCAGAAAGAACTCGTCAAGAGCGGA 3507
Db 2096 AAATACCGCATCAGAAATTTGTAAGCGTTAATAATTCAGAAAGAACTCGTCAAGAGCGGA 2155
Qy 3508 TAGAAGCGGATCGCTCGAATCGGAGCGGATACCGTAAAGCAAGAGAGCGGTCA 3567
Db 2156 TAGAAGCGGATCGCTCGAATCGGAGCGGATACCGTAAAGCAAGAGAGCGGTCA 2215
Qy 3568 GCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCAACGCTATGCTCTGTATAG 3627
Db 2216 GCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCAACGCTATGCTCTGTATAG 2275
Qy 3628 CGGTCCGGCACACCGAGCGGCCACAGTCGATGAATCCAGAAAGCGGCCATTTTCCACC 3687
Db 2276 CGGTCCGGCACACCGAGCGGCCACAGTCGATGAATCCAGAAAGCGGCCATTTTCCACC 2335
Qy 3688 ATGATATTTCGCAAGCAGGATCGCATGGTTCAGCAGAGATCCTCGCGTCGGGATG 3747
Db 2336 ATGATATTTCGCAAGCAGGATCGCATGGTTCAGCAGAGATCCTCGCGTCGGGATG 2395
Qy 3748 CTCGCCCTTGAGCTTGGCGAAACAGTTTCGGCTGGCGGAGCCCTGATGCTCTTCGTCGAGA 3807
Db 2396 CTCGCCCTTGAGCTTGGCGAAACAGTTTCGGCTGGCGGAGCCCTGATGCTCTTCGTCGAGA 2455
Qy 3808 TCATCTCGATCGAAGACCGGCTTCATTCGAGTAGCTGCTCGCTCGATGCGATGTTTC 3867
Db 2456 TCATCTCGATCGAAGACCGGCTTCATTCGAGTAGCTGCTCGCTCGATGCGATGTTTC 2515
Qy 3868 GTTGTGTGTGCAATGGGAGGATAGCGGATCAAGCGTATGCGAGCGCGCGCATTTGATCA 3927
Db 2516 GTTGTGTGTGCAATGGGAGGATAGCGGATCAAGCGTATGCGAGCGCGCGCATTTGATCA 2575
Qy 3928 GCCATGATGATATCTTTCTCGGCAAGGAGCAAGGTGAGATGACAGAGATCCTGCCCCGGC 3987
Db 2576 GCCATGATGATATCTTTCTCGGCAAGGAGCAAGGTGAGATGACAGAGATCCTGCCCCGGC 2635
Qy 3988 ACTTCGCCCAATAGCAGCGAGTCCCTTCCCGCTTCAGTGACAGCGTCGAGCAAGCTGCG 4047
Db 2636 ACTTCGCCCAATAGCAGCGAGTCCCTTCCCGCTTCAGTGACAGCGTCGAGCAAGCTGCG 2695
Qy 4048 CAAGGAACCGCGCTGTTGGCGAGCCAGATAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 4107
Db 2696 CAAGGAACCGCGCTGTTGGCGAGCCAGATAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 2755
Qy 4108 AGGCAACCGGACAGGTCTGTTGACAAAAGAACCGGGGCGCCCTGCTGCTGACAGCGCG 4167
Db 2756 AGGCAACCGGACAGGTCTGTTGACAAAAGAACCGGGGCGCCCTGCTGCTGACAGCGCG 2815
Qy 4168 AACAGCGGGGATCAGAGAGCGGATGCTGTTGTCGCCAGTCATAGCGGAATAGGCTC 4227
Db 2816 AACAGCGGGGATCAGAGAGCGGATGCTGTTGTCGCCAGTCATAGCGGAATAGGCTC 2875
Qy 4228 TCAACCAAGCGGCGGAGAACCTGCGTGCAATCCATCTTGTTCATATCATCGGAACGAT 4287
Db 2876 TCAACCAAGCGGCGGAGAACCTGCGTGCAATCCATCTTGTTCATATCATCGGAACGAT 2935
Qy 4288 CCTCATCTGTCTTTCATCAGAGCTTGATCCCTTCGCCCATCAG 4332
Db 2936 CCTCATCTGTCTTTCATCAGAGCTTGATCCCTTCGCCCATCAG 2980
```

RESULT 10

```
US-09-484-317A-19
; Sequence 19, Application US/09484317A
; Patent No. 6740503
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: ATX-007CP4DV11
; CURRENT APPLICATION NUMBER: US/09/484,317A
; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 4644
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-484-317A-19
```

```
Query Match 36.6%; Score 1586.2; DB 3; Length 4644;
Best Local Similarity 96.0%; Pred. No. 2.8e-258;
Matches 1656; Conservative 0; Mismatches 23; Indels 46; Gaps 1;

Qy 2608 CATGTGAGCAAAAGGCGCAGCAAAAGGCGCAAGAACCGGTAAAGAGCCCGTGTGCGGCTT 2667
Db 1302 CATGTGAGCAAAAGGCGCAGCAAAAGGCGCAGCAAAAGGCGCGTGTGCGGCTT 1361
Qy 2668 TTTCCATAGGCTCCGCCCGCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTG 2727
Db 1362 TTTCCATAGGCTCCGCCCGCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTG 1421
Qy 2728 GCGAAACCGCGACAGGACTATAAAGATACCAAGCGGTTTCCCGCTGGAAGCTCCCTCGTSCG 2787
Db 1422 GCGAAACCGCGACAGGACTATAAAGATACCAAGCGGTTTCCCGCTGGAAGCTCCCTCGTSCG 1481
Qy 2788 CTCTCTGTTCGACCGCTTACCGGATACCTGTGCGGCTTCTCCCTTCGCGGAAG 2847
Db 1482 CTCTCTGTTCGACCGCTTACCGGATACCTGTGCGGCTTCTCCCTTCGCGGAAG 1541
Qy 2848 CGTGGCGCTTCTCAATGCTCAGCTGTAGGTATCTCAGTTCCGTTGAGTTCGCTC 2907
Db 1542 CGTGGCGCTTCTCAATGCTCAGCTGTAGGTATCTCAGTTCCGTTGAGTTCGCTC 1601
Qy 2908 CAAAGCTGGGCTGTGTGCAAGAACCCCGCTTACGCGCGAGCCGCTGCGGCTTATCCGGTAA 2967
Db 1602 CAAAGCTGGGCTGTGTGCAAGAACCCCGCTTACGCGCGAGCCGCTGCGGCTTATCCGGTAA 1661
Qy 2968 CTATCTCTTGTAGTCAACCCCGGTAAAGACAGCATTTATCGCCACTGCGCAGCAGCACTGG 3027
Db 1662 CTATCTCTTGTAGTCAACCCCGGTAAAGACAGCATTTATCGCCACTGCGCAGCAGCACTGG 1721
Qy 3028 TAACAGATTAGCAGAGCGAGGTATGTAGCGGTGTCTACAGAGTCTTGAAGTGGTGGCC 3087
Db 1722 TAACAGATTAGCAGAGCGAGGTATGTAGCGGTGTCTACAGAGTCTTGAAGTGGTGGCC 1781
Qy 3088 TAACTACGGCTACACTAGAAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTAC 3147
Db 1782 TAACTACGGCTACACTAGAAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTAC 1841
Qy 3148 CTTTCGGAAGAGTTGGTAGCTCTTGTATCCGCAACCAACCAACCGCTGGTAGCGGTGG 3207
Db 1842 CTTTCGGAAGAGTTGGTAGCTCTTGTATCCGCAACCAACCAACCGCTGGTAGCGGTGG 1901
```


QY 3148 CTTCCGAAAGAGTTGGTAGCTCTTGATCCGGCAAAACCAACACCGCTGGTAGCGGTG 3207
DB 1842 CTTCCGAAAGAGTTGGTAGCTCTTGATCCGGCAAAACCAACCGCTGGTAGCGGTG 1901
QY 3208 TTTTGTGTTGCAAGCAGCAGATTA CGCGCAGAAAAAAGGATCTCAAGAAGATCCTTT 3267
DB 1902 TTTTGTGTTGCAAGCAGCAGATTA CGCGCAGAAAAAAGGATCTCAAGAAGATCCTTT 1961
QY 3268 GATCTTTTCTACGGGTCTGACGCTCAGTGGAGGAAACTCAGTTAAAGGATTTGGT 3327
DB 1962 GATCTTTTCTACGGGTCTGACGCTCAGTGGAGGAAACTCAGTTAAAGGATTTGGT 2021
QY 3328 CATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAATAGGGGTTCGCGCAC 3387
DB 2022 CATGAGATTATCAAAAAGGATCTTCACTAGA----- 2053
QY 3388 ATTTCCCGAAAGTGCACCTGTATCGGTGTGAATATACGACAGATCGGTAAGAGA 3447
DB 2054 -----TCCTTTATCGGTGTGAATATACGACAGATCGGTAAGAGA 2095
QY 3448 AAATACCGCATCAGAAATGTAAGCTTAATATTCAGAGAACTCGTCAAGAGCGGA 3507
DB 2096 AAATACCGCATCAGAAATGTAAGCTTAATATTCAGAGAACTCGTCAAGAGCGGA 2155
QY 3508 TAGAAGCGGATCGCTCGGAATCGGAGCGCGATACCGTAAAGCAGGAAAGCGGTCA 3567
DB 2156 TAGAAGCGGATCGCTCGGAATCGGAGCGCGATACCGTAAAGCAGGAAAGCGGTCA 2215
QY 3568 GCCCATTCGCGGCAAGCTTTACGAAATATACGGGTAGCCAAAGCTATGTCTGTATAG 3627
DB 2216 GCCCATTCGCGGCAAGCTTTACGAAATATACGGGTAGCCAAAGCTATGTCTGTATAG 2275
QY 3628 CGGTCCGACACCCAGCGGCGCACAGTGCATGAATCCAGAAAGCGGCAATTTCCACC 3687
DB 2276 CGGTCCGACACCCAGCGGCGCACAGTGCATGAATCCAGAAAGCGGCAATTTCCACC 2335
QY 3688 ATGATATTCGGCAAGCAGGATCGCCATCGGATCACGACGAGATCCTCGCGCTCGGCGATG 3747
DB 2336 ATGATATTCGGCAAGCAGGATCGCCATCGGATCACGACGAGATCCTCGCGCTCGGCGATG 2395
QY 3748 CTGCGCTTGAGCTTGGGAAACAGTTGGTGGCGGAGGCCCTGTATGCTTTCTGTCAGA 3807
DB 2396 CTGCGCTTGAGCTTGGGAAACAGTTGGTGGCGGAGGCCCTGTATGCTTTCTGTCAGA 2455
QY 3808 TCATCTGTATCGCAAGACCGGCTTCCATCCGAGTAGCTGCTCGCTCGATGCGATGTTTC 3867
DB 2456 TCATCTGTATCGCAAGACCGGCTTCCATCCGAGTAGCTGCTCGCTCGATGCGATGTTTC 2515
QY 3868 GCTTGTGTGTCGAATGGGCAAGTAGCGGATCAAGCGTATGACGCGCGCCCATTTGCATCA 3927
DB 2516 GCTTGTGTGTCGAATGGGCAAGTAGCGGATCAAGCGTATGACGCGCGCCCATTTGCATCA 2575
QY 3928 GCATGATGATATTTCTCGGAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCGCGG 3987
DB 2576 GCATGATGATATTTCTCGGAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCGCGG 2635
QY 3988 ACTTCCGCCAATAGCAGCAGTCCCTTCCCGCTTTCAGTGACACGTCGAGCAGCTGG 4047
DB 2636 ACTTCCGCCAATAGCAGCAGTCCCTTCCCGCTTTCAGTGACACGTCGAGCAGCTGG 2695
QY 4048 CAAGGAACCGCTCGTGGCAGCCACGATAGCGGCTGCGCTCTGCTTTGCACTTCAATTC 4107
DB 2696 CAAGGAACCGCTCGTGGCAGCCACGATAGCGGCTGCGCTCTGCTTTGCACTTCAATTC 2755
QY 4108 AGGCGCACCGACAGTGGTCTTGACAAAAGAAACCGGGCGCCCTCGCTGACGCGG 4167
DB 2756 AGGCGCACCGACAGTGGTCTTGACAAAAGAAACCGGGCGCCCTCGCTGACGCGG 2815
QY 4168 AACACGCGGCATCAGACGAGCGGATTTGCTGTTGTGCGCAGTCATAGCGGATAGCTTC 4227
DB 2816 AACACGCGGCATCAGACGAGCGGATTTGCTGTTGTGCGCAGTCATAGCGGATAGCTTC 2875

QY 4228 TCACCCCAAGCGCGGAGAACCTCGTGCATCCATCTTTCAATCATGTCGAAACGAT 4287
DB 2876 TCACCCCAAGCGCGGAGAACCTCGTGCATCCATCTTTCAATCATGTCGAAACGAT 2935
QY 4288 CCTCATCTGTCTCTTTGATCAGAGCTTTGATCCCTCTGCGCATCAG 4332
DB 2936 CCTCATCTGTCTCTTTGATCAGAGCTTTGATCCCTCTGCGCATCAG 2980

RESULT 12
US-09-479-122-20
; Sequence 20, Application US/09479122
; Patent No. 6410266
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003C
; CURRENT APPLICATION NUMBER: US/09/479,122
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 5247
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-479-122-20

Query Match 36.6%; Score 1586.2; DB 3; Length 5247;
Best Local Similarity 96.0%; Pred. No. 2.8e-258;
Matches 1656; Conservative 0; Mismatches 23; Indels 46; Gaps 1;

QY 2608 CATGTGAGCAAAAGGCGCAGAAAGCCAGGACCGTAAAGGCGCGCTTGTGGCGTT 2667
DB 1250 CATGTGAGCAAAAGGCGCAGAAAGCCAGGACCGTAAAGGCGCGCTTGTGGCGTT 1309
QY 2668 TTTTCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTG 2727
DB 1310 TTTTCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTG 1369
QY 2728 GCGAAACCGCAGCAGGACTATAAGATACAGGCGTTTCCCTCGGAAGCTCCCTCGTGG 2787
DB 1370 GCGAAACCGCAGCAGGACTATAAGATACAGGCGTTTCCCTCGGAAGCTCCCTCGTGG 1429
QY 2788 CTCTCTGTTCGACCGCTTACCGGATACCTGCGGCTTCTCCCTTCGGGAAG 2847
DB 1430 CTCTCTGTTCGACCGCTTACCGGATACCTGCGGCTTCTCCCTTCGGGAAG 1489
QY 2848 CGTGGCGCTTTCTCAATGCTCAGCTGTAGGTATCTCAGTTGGGTAGGTCTGTCGCTC 2907
DB 1490 CGTGGCGCTTTCTCAGCTCAGCTGTAGGTATCTCAGTTGGGTAGGTCTGTCGCTC 1549
QY 2908 CAAAGCTGGCTGTGTGACAGAAACCCCGCTTACGCGCGACCGCTGGCGCTTATCCGGTAA 2967
DB 1550 CAAAGCTGGCTGTGTGACAGAAACCCCGCTTACGCGCGACCGCTGGCGCTTATCCGGTAA 1609
QY 2968 CTATCTGTCTTGTAGTCAACCCCGCTTAAGACACGACTTATCGCACCTGGCAGCAGCTCG 3027
DB 1610 CTATCTGTCTTGTAGTCAACCCCGCTTAAGACACGACTTATCGCACCTGGCAGCAGCTCG 1669
QY 3028 TAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTCTGAAGTGTGGCC 3087

1670 TAA CAGGATTAGCAGACGAGGATATGTAGCGGTGCTACAGAGTTCTTTGAAGTGTGGCC 1729
3088 TAACTACGGCTACACTAGAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTAC 3147
1730 TAACTACGGCTACACTAGAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTAC 1789
3148 CTTCCGAAAAAGCTTGGTAGCTTTGATCCGGCAAAACAAACCAACCGCTGCTAGCGGTGG 3207
1790 CTTCCGAAAAAGCTTGGTAGCTTTGATCCGGCAAAACAAACCAACCGCTGCTAGCGGTGG 1849
3208 TTTTCTTTGTTGCAAGCAGCAGATTAACCGCAGAAAAAAGGATCTCAAGAGATCTCTTT 3267
1850 TTTTCTTTGTTGCAAGCAGCAGATTAACCGCAGAAAAAAGGATCTCAAGAGATCTCTTT 1909
3268 GATCTTTCTACGGGTCTGACGCTCAGTGGAGCGAAACCTCACGTTAAAGGATTTTGGT 3327
1910 GATCTTTCTACGGGTCTGACGCTCAGTGGAGCGAAACCTCACGTTAAAGGATTTTGGT 1969
3328 CATGAGCGATACATATTTGAATGTATTTGAAAAATAAAACAAATAGGGTTCCGCGCAC 3387
1970 CATGAGATTACAAAGGATCTTCACTAGA----- 2001
3388 ATTTCCCGAAAAAGTGCACCTGTATGCGGTGTGAATAACCGCACAGATCGTTAAGGAGA 3447
2002 -----TCCTTTTATCGGTGTGAAATATACCGCACAGATCGTTAAGGAGA 2043
3448 AAATACCGCATCAGGAATCTAGCGTTAATAATTCAGAGAACTCGTCAAGAAAGCGA 3507
2044 AAATACCGCATCAGGAATCTAGCGTTAATAATTCAGAGAACTCGTCAAGAAAGCGA 2103
3508 TAGAAGCGATGCGTGCATTCGGAGCGCGGATACCGTTAAGCAGGAGAAAGCGGTCA 3567
2104 TAGAAGCGATGCGTGCATTCGGAGCGCGGATACCGTTAAGCAGGAGAAAGCGGTCA 2163
3568 GCCATTCCGCGCCAGCTCTTACGATATATACGGGTAGGCAAGCTATGCTCGTAGAG 3627
2164 GCCATTCCGCGCCAGCTCTTACGATATATACGGGTAGGCAAGCTATGCTCGTAGAG 2223
3628 CGGTCCGCGCACACCGCGCGCACAGTTCGATGAATCCAGAAAGCGGCCATTTTCCACC 3687
2224 CGGTCCGCGCACACCGCGCGCACAGTTCGATGAATCCAGAAAGCGGCCATTTTCCACC 2283
3688 ATGATATTCCGACAGCAGCATTCGATGGGTACGACAGATCTCCGCGTCCGGCATG 3747
2284 ATGATATTCCGACAGCAGCATTCGATGGGTACGACAGATCTCCGCGTCCGGCATG 2343
3748 CTCGCTTGGCTGCGAAGCAGTTTCGGTGGCGGAGCCCTGATGCTCTCGTCCAGA 3807
2344 CTCGCTTGGCTGCGAAGCAGTTTCGGTGGCGGAGCCCTGATGCTCTCGTCCAGA 2403
3808 TCATCTCTGATCGACAAGACCGGCTTCCATCCGAGTACGTCGCTCGATGCGATGTTTC 3867
2404 TCATCTCTGATCGACAAGACCGGCTTCCATCCGAGTACGTCGCTCGATGCGATGTTTC 2463
3868 GCTTGGTGGTTCGAAATGGGAGGTAGCCGATCAAGCGTATGACGCGCGCATTCGATCA 3927
2464 GCTTGGTGGTTCGAAATGGGAGGTAGCCGATCAAGCGTATGACGCGCGCATTCGATCA 2523
3928 GCATGATGATATCTTTCGCGAGGACAGGTGAGATGACAGAGATCTTCCGCGCGC 3987
2524 GCATGATGATATCTTTCGCGAGGACAGGTGAGATGACAGAGATCTTCCGCGCGC 2583
3988 ACTTCGCGCAATAGCAGCGAGTCCCTTCCCGCTTCAGTGACAAACGTCGAGCACAGTGG 4047
2584 ACTTCGCGCAATAGCAGCGAGTCCCTTCCCGCTTCAGTGACAAACGTCGAGCACAGTGG 2643
4048 CAAGGAAACCGCGCTGCTGGCCAGCACGATAGCGCGCTGCTCTTGGAGTTTCATTC 4107
2644 CAAGGAAACCGCGCTGCTGGCCAGCACGATAGCGCGCTGCTCTTGGAGTTTCATTC 2703
4108 ACGGACCGGACAGGTTCGCTTTGACAAAAAGAACCGGCGCGCCCTGCGCTCAGACCGCG 4167

2704 AGGCGACCGGACAGGTCTGCTTGCACAAAAAGAACCGGGGCGCCCTGCGCTGACACCGG 2763
4168 AACACGCGCGCATCAGAGCAGCCGATTTGTTGTGCCAGTCAATAGCCGAATAGCCTC 4227
2764 AACACGCGCGCATCAGAGCAGCCGATTTGTTGTGCCAGTCAATAGCCGAATAGCCTC 2823
4228 TCACACCAAGCGCGGAGAACCTCGTGCAATCCATCTTGTTCATCATCGGAAACGAT 4287
2824 TCACACCAAGCGCGGAGAACCTCGTGCAATCCATCTTGTTCATCATCGGAAACGAT 2883
4288 CCTCATCTCTCTCTTCATCAGAGCTTGATCCCTCGGCCATCAG 4332
2884 CCTCATCTCTCTCTTCATCAGAGCTTGATCCCTCGGCCATCAG 2928

RESULT 13
US-09-484-997-20
; Sequence 20, Application US/09484997
; Patent No. 6524818
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003J
; CURRENT APPLICATION NUMBER: US/09/484,997
; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 20
; LENGTH: 5247
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-484-997-20

Query Match 36.6%; Score 1586.2; DB 3; Length 5247;
Best Local Similarity 96.0%; Pred. No. 2.8e-258;
Matches 1656; Conservative 0; Mismatches 23; Indels 46; Gaps 1;

QY 2608 CATGTGACAAAGGCGCAGCAAAAGGCGCAGGAAACCGTAAAAAGGCGGTTGCTGGCGTT 2667
DB 1250 CATGTGACAAAGGCGCAGCAAAAGGCGCAGGAAACCGTAAAAAGGCGGTTGCTGGCGTT 1309
QY 2668 TTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCAGCCTCAAGTCAGAGGTG 2727
DB 1310 TTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCAGCCTCAAGTCAGAGGTG 1369
QY 2728 GCGAAACCGCAGCAGGACTATAAAGATACAGGCGTTTCCCTCGGAAGCTCCCTCGTGG 2787
DB 1370 GCGAAACCGCAGCAGGACTATAAAGATACAGGCGTTTCCCTCGGAAGCTCCCTCGTGG 1429
QY 2788 CTCTCTGTTCCGACCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAG 2847
DB 1430 CTCTCTGTTCCGACCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAG 1489
QY 2848 CGTGGCGTTTCTCAATGCTCAGCTGAGGTATCTCAGTTGCTGCTGAGTGTGCTTC 2907
DB 1490 CGTGGCGTTTCTCAATGCTCAGCTGAGGTATCTCAGTTGCTGCTGAGTGTGCTTC 1549
QY 2908 CAAGCTGGGCTGTGTGACAGAACCCCGCTTCAGCCGACCGCTGCGCTTATCCGGTAA 2967
DB 1550 CAAGCTGGGCTGTGTGACAGAACCCCGCTTCAGCCGACCGCTGCGCTTATCCGGTAA 1609

Qy 2968 CTATCGTCTTGGTCCAAACCGGTAAAGACAGCACTTATCGCACTGGCAGCAGCACTGG 3027
 Db 1610 CTATCGTCTTGGTCCAAACCGGTAAAGACAGCACTTATCGCACTGGCAGCAGCACTGG 1669
 Qy 3028 TAAACAGATTAAGACAGAGAGGATATGATGCGGTGCTACAGAGTCTTGAAGTGGTGGCC 3087
 Db 1670 TAAACAGATTAAGACAGAGAGGATATGATGCGGTGCTACAGAGTCTTGAAGTGGTGGCC 1729
 Qy 3088 TAACTACGGCTACACTAGAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTAC 3147
 Db 1730 TAACTACGGCTACACTAGAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTAC 1789
 Qy 3148 CTTCCGAAAAGAGTTGGTATCTTGTATCCGCGCAAAACCAACCCCTGCTAGCGGTGG 3207
 Db 1790 CTTCCGAAAAGAGTTGGTATCTTGTATCCGCGCAAAACCAACCCCTGCTAGCGGTGG 1849
 Qy 3208 TTTTCTTTGTTTGAAGCAGAGATTAAGCGCAGAAAAAAGATCTCAAGAAATCTTTT 3267
 Db 1850 TTTTCTTTGTTTGAAGCAGAGATTAAGCGCAGAAAAAAGATCTCAAGAAATCTTTT 1909
 Qy 3268 GATCTTTTCTACGGGCTGACGCTCAGTGAAGCAAAACCTCAAGTTAAGGATTTTGGT 3327
 Db 1910 GATCTTTTCTACGGGCTGACGCTCAGTGAAGCAAAACCTCAAGTTAAGGATTTTGGT 1969
 Qy 3328 CATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAAACAAATAGGGGTTCGCGCAC 3387
 Db 1970 CATGAGATTAACAAAGGATCTTCACTAGA----- 2001
 Qy 3388 ATTTCCCGAAAGTGCACCTGTATGCGGTGTAATACCGCACAGATCGGTAAGAGA 3447
 Db 2002 -----TCCCTTTATCGGTGTGAATATCGGCATACCGCACAGATCGGTAAGAGA 2043
 Qy 3448 AATACCGCATCAGAAATGTAAGCTTAATATTCAGAGAACTCGTCAAGAGCGCA 3507
 Db 2044 AATACCGCATCAGAAATGTAAGCTTAATATTCAGAGAACTCGTCAAGAGCGCA 2103
 Qy 3508 TAGAAGCGGATCGCTCGAATCGGAGCGCGCATACCGTAAAGCAGAGAGCGGTCA 3567
 Db 2104 TAGAAGCGGATCGCTCGAATCGGAGCGCGCATACCGTAAAGCAGAGAGCGGTCA 2163
 Qy 3568 GCCATTTCCGCGCAAGCTCTTACGAATATACGGGTAGCAAGCTATGCTCTGTATAG 3627
 Db 2164 GCCATTTCCGCGCAAGCTCTTACGAATATACGGGTAGCAAGCTATGCTCTGTATAG 2223
 Qy 3628 CGTCCGCGCACACCCAGCGGACAGTCCGATGAATCCAGAAAGCGGCCATTTCCACC 3687
 Db 2224 CGTCCGCGCACACCCAGCGGACAGTCCGATGAATCCAGAAAGCGGCCATTTCCACC 2283
 Qy 3688 ATGATATTCGCAAGCAGGATCGCCATGGTTCACGACGAGATCCTCGCGTGGGCGATG 3747
 Db 2284 ATGATATTCGCAAGCAGGATCGCCATGGTTCACGACGAGATCCTCGCGTGGGCGATG 2343
 Qy 3748 CTGCGCTTGGCTGGCGCAAGTTCGGCTGGCGGAGCGCCCTGATGCTCTTGTTCAGA 3807
 Db 2344 CTGCGCTTGGCTGGCGCAAGTTCGGCTGGCGGAGCGCCCTGATGCTCTTGTTCAGA 2403
 Qy 3808 TCATCTGTATGCAACAGACCGGCTTCCATCCGAGTACGTCTCGCTCGATGCCATGTTTC 3867
 Db 2404 TCATCTGTATGCAACAGACCGGCTTCCATCCGAGTACGTCTCGCTCGATGCCATGTTTC 2463
 Qy 3868 GCTTGGTGGTGAATGGGCGAGGTAGCCGATCAAGCGTATGCAAGCCGCCCATTTGCATCA 3927
 Db 2464 GCTTGGTGGTGAATGGGCGAGGTAGCCGATCAAGCGTATGCAAGCCGCCCATTTGCATCA 2523
 Qy 3928 GCCATGATGATATTTCTCGGAGGAGCAAGTGATGATGACAGGAGATCTTCCCGCGG 3987
 Db 2524 GCCATGATGATATTTCTCGGAGGAGCAAGTGATGATGACAGGAGATCTTCCCGCGG 2583
 Qy 3988 ACTTCGCCCAATAGCAGCAGTCCCTTCCCGCTTCAAGTGAACAGTGCAGCAGAGTGGC 4047
 Db 2584 ACTTCGCCCAATAGCAGCAGTCCCTTCCCGCTTCAAGTGAACAGTGCAGCAGAGTGGC 2643

Qy 4048 CAAGGAACGCCCGTCTGCGCCAGCAGCAGTAGCCGCGCTGCTTTCAGTTCATTTC 4107
 Db 2644 CAAGGAACGCCCGTCTGCGCCAGCAGCAGTAGCCGCGCTGCTTTCAGTTCATTTC 2703
 Qy 4108 AGGGCACCGGACAGGTTCGTTGACAAAAAAGAACCGGGCGCCCTGCGCTGACAGCCGG 4167
 Db 2704 AGGGCACCGGACAGGTTCGTTGACAAAAAAGAACCGGGCGCCCTGCGCTGACAGCCGG 2763
 Qy 4168 AACACCGCGCATCAGAGCAGCGGATTTGCTGTTGTGCCAGTCATAGCCGAATAGCCTC 4227
 Db 2764 AACACCGCGCATCAGAGCAGCGGATTTGCTGTTGTGCCAGTCATAGCCGAATAGCCTC 2823
 Qy 4228 TCCACCAAGCGCGGAGAACCTGCGTGCATATCCATCTTGTTCATATCATCGCAACGAT 4287
 Db 2824 TCCACCAAGCGCGGAGAACCTGCGTGCATATCCATCTTGTTCATATCATCGCAACGAT 2883
 Qy 4288 CCTCATCTCTCTCTTGTATCAGAGCTTGATCCCTCTGGCCCATCAG 4332
 Db 2884 CCTCATCTCTCTCTTGTATCAGAGCTTGATCCCTCTGGCCCATCAG 2928

RESULT 14
 US-09-481-355-20
 ; Sequence 20, Application US/09481355
 ; Patent No. 6524824
 ; GENERAL INFORMATION:
 ; APPLICANT: HARRINGTON, JOHN J.
 ; APPLICANT: SHERP, BRUCE
 ; APPLICANT: RUNDLETT, STEPHEN
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
 ; TITLE OF INVENTION: ENDOGENOUS GENES
 ; FILE REFERENCE: 0221-0003F
 ; CURRENT APPLICATION NUMBER: US/09/481,355
 ; CURRENT FILING DATE: 2000-01-12
 ; PRIOR APPLICATION NUMBER: 09/276,820
 ; PRIOR FILING DATE: 1999-03-26
 ; PRIOR APPLICATION NUMBER: 09/159,643
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 08/941,223
 ; PRIOR FILING DATE: 1997-09-26
 ; PRIOR APPLICATION NUMBER: 09/263,814
 ; PRIOR FILING DATE: 1999-03-08
 ; PRIOR APPLICATION NUMBER: 09/253,022
 ; PRIOR FILING DATE: 1999-02-19
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 20
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-481-355-20

Query Match 36.8%; Score 1586.2; DB 3; Length 5247;
 Best Local Similarity 96.0%; Pred. No. 2.8e-258;
 Matches 1656; Conservative 0; Mismatches 23; Indels 46; Gaps 1;
 Qy 2608 CATGTGAGCAAAAGGCGCAGCAAAAGCGCAGAACCGTAAAGAGCGCGCTTGTGGCGTT 2667
 Db 1250 CATGTGAGCAAAAGGCGCAGCAAAAGCGCAGAACCGTAAAGAGCGCGCTTGTGGCGTT 1309
 Qy 2668 TTTTCATAGGCTCCGCCCTCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTG 2727
 Db 1310 TTTTCATAGGCTCCGCCCTCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTG 1369
 Qy 2728 GCCAAACCGCAGAGGACTATAAGATACGAGGCTTCCCTCGGAGCTCCCTCGTGCG 2787
 Db 1370 GCCAAACCGCAGAGGACTATAAGATACGAGGCTTCCCTCGGAGCTCCCTCGTGCG 1429
 Qy 2788 CTCTCTGTTTCCGACCTTCGCGTTACCGGATACCTGTCCGCTTTTCTCCCTTCGGGAAG 2847
 Db 1430 CTCTCTGTTTCCGACCTTCGCGTTACCGGATACCTGTCCGCTTTTCTCCCTTCGGGAAG 1489
 Qy 2848 CGTGGCGCTTTTCTCAATGCTCAGCTGATAGGTATCTCAGTTCGGTGTAGGTGCTCCTC 2907

Db 1490 |||||CGTGGCGCTTCTCATAGCTCAGCGTGTAGGTATCTCAGTTTCGGTGTAGGTCTCGTCTC 1549
Qy 2908 CAAGCTGGGCTGTGTGACGAACCCCGTTTCAGCCGACCGCTGTGCGCTTATCCGGTAA 2967
Db 1550 |||||CGTGGCTGTGTGACGAACCCCGTTTCAGCCGACCGCTGTGCGCTTATCCGGTAA 1609
Qy 2968 CTATCGTCTTTCAGTTCACCCGGTAAAGACAGACTTATCGCACCTGGCGAGCAGCACTGG 3027
Db 1610 CTATCGTCTTTCAGTTCACCCGGTAAAGACAGACTTATCGCACCTGGCGAGCAGCACTGG 1669
Qy 3028 TAAACAGGATAGCAGAGCGAGTATAGGCGGTGCTACAGAGTCTTGAAGTGTGGCC 3087
Db 1670 TAAACAGGATAGCAGAGCGAGTATAGGCGGTGCTACAGAGTCTTTCGAAGTGTGGCC 1729
Qy 3088 TAACTACCGCTACACTAGAGCAGAGTATTTGGTATCTGCGCTCTGCTGAAGCAGATTAC 3147
Db 1730 TAACTACCGCTACACTAGAGCAGAGTATTTGGTATCTGCGCTCTGCTGAAGCAGATTAC 1789
Qy 3148 CTTTCGAAAAAGAGTTGGTGTCTTTGATCCGGCAAAACAAACCCGCTGTGTAGCGTGG 3207
Db 1790 CTTTCGAAAAAGAGTTGGTGTCTTTGATCCGGCAAAACAAACCCGCTGTGTAGCGTGG 1849
Qy 3208 TTTTTCGTTTTCAGAGCAGAGTATTCAGCGCAGAAAAAGAGTCTCAAGAGATCTTT 3267
Db 1850 TTTTTCGTTTTCAGAGCAGAGTATTCAGCGCAGAAAAAGAGTCTCAAGAGATCTTT 1909
Qy 3268 GATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAACTCAGCTTAAGGATTTTGGT 3327
Db 1910 GATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAACTCAGCTTAAGGATTTTGGT 1969
Qy 3328 CATGAGCGGATACATATTTGAATGTATTTAGAAAAATAACAAATAGGGTTTCGCGCAC 3387
Db 1970 CATGAGATTTACAAAAGAGTCTTACCTAGA----- 2001
Qy 3388 ATTTCCCGAAAAGTCCACCTGTATCGGTGTGAATACCGCAGAGTGGTAAGGAGA 3447
Db 2002 -----TCCTTTTATCGGTGTGAATACCGCAGAGTGGTAAGGAGA 2043
Qy 3448 AAATACCGCATCAGGAATTTGAAGCTTAATTAATTCAGAGAACTCGTCAAGAGGCGA 3507
Db 2044 AAATACCGCATCAGGAATTTGAAGCTTAATTAATTCAGAGAACTCGTCAAGAGGCGA 2103
Qy 3508 TAGAAGGCGATCGCTGCGAATCGGAGCGGCGATACCGTAAAGCAGAGGAAGCGGTCA 3567
Db 2104 TAGAAGGCGATCGCTGCGAATCGGAGCGGCGATACCGTAAAGCAGAGGAAGCGGTCA 2163
Qy 3568 GCCATTTCGCGCGCAAGCTCTTCAGCAATATCAGCGGTAGCCACGCTATGTCTTGATAG 3627
Db 2164 GCCCATTCGCGCGCAAGCTCTTCAGCAATATCAGCGGTAGCCACGCTATGTCTTGATAG 2223
Qy 3628 CGTTCGCGCACACCCAGCGCGCACAGTTCGATGAATCCAGAAAAAGCGGCAATTTTCCACC 3687
Db 2224 CGTTCGCGCACACCCAGCGCGCACAGTTCGATGAATCCAGAAAAAGCGGCAATTTTCCACC 2283
Qy 3688 ATGATATTCGGAAGCAGGATCGCCATGGGTCAACAGAGATCTTCGCGCTCGGCGCATG 3747
Db 2284 ATGATATTCGGAAGCAGGATCGCCATGGGTCAACAGAGATCTTCGCGCTCGGCGCATG 2343
Qy 3748 CTGCGCTTCGAGCTCGGCAACAGTTCGCTGCGCGAGCCCTGATGCTCTTCGTCAGA 3807
Db 2344 CTGCGCTTCGAGCTCGGCAACAGTTCGCTGCGCGAGCCCTGATGCTCTTCGTCAGA 2403
Qy 3808 TCATCTTCGATCGAACAGACCGGCTTCATCCGAGTACGTGCTGCTCGATGCGATGTTTC 3867
Db 2404 TCATCTTCGATCGAACAGACCGGCTTCATCCGAGTACGTGCTGCTCGATGCGATGTTTC 2463
Qy 3868 GCTTGTGTGCGAATGGGAGGATAGCCGATCAGCGGTATGACCGCGCGCATTCGATCA 3927
Db 2464 GCTTGTGTGCGAATGGGAGGATAGCCGATCAGCGGTATGACCGCGCGCATTCGATCA 2523
Qy 3928 GCATCATGGATCTTCTCGGAGGAGCAAGGTGAGATGACAGGAGATCTTCGCCCGCGC 3987

Db 2524 GCCATGATGATATCTTCTCGGCGAGGAGCAAGGTGAGATGACAGGAGATCTCTGCCCGGC 2583
Qy 3988 ACTTCGCCCAATAGCAGCCAGTCCCTTTCCGCTTTCAGTGACAAAGTTCGAGCAGCTGCG 4047
Db 2584 ACTTCGCCCAATAGCAGCCAGTCCCTTTCCGCTTTCAGTGACAAAGTTCGAGCAGCTGCG 2643
Qy 4048 CAAGGAACGCCGCTGCTGGCCAGCAGCAGATAGCGCGCTGCTGCTTCGAGTTCATTC 4107
Db 2644 CAAGGAACGCCGCTGCTGGCCAGCAGCAGATAGCGCGCTGCTGCTTCGAGTTCATTC 2703
Qy 4108 AGGSCACCGCAGACGTCGCTTTCACAAAAAGAACCGGCGCCCTGCGCTGACAGCGCG 4167
Db 2704 AGGSCACCGCAGACGTCGCTTTCACAAAAAGAACCGGCGCCCTGCGCTGACAGCGCG 2763
Qy 4168 AACACGCGCGCATCAGAGCAGCCGATTTGTCTGTGTGCCAGTATAGCCGAATAGCCTC 4227
Db 2764 AACACGCGCGCATCAGAGCAGCCGATTTGTCTGTGTGCCAGTATAGCCGAATAGCCTC 2823
Qy 4228 TCCACCCAGCGCGCGAGACCTGCGTGAATCCATCTTGTTCATCATCGGAAACGAT 4287
Db 2824 TCCACCCAGCGCGCGAGAACCTGCGTGAATCCATCTTGTTCATCATCGGAAACGAT 2883
Qy 4288 CCTCATCTGCTCTTGTATCAGAGCTTGATCCCTGCGCCATCAG 4332
Db 2884 CCTCATCTGCTCTTGTATCAGAGCTTGATCCCTGCGCCATCAG 2928

RESULT 15
US-09-481-282-20
; Sequence 20, Application US/09481282
; Patent No. 6541221
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-000305
; CURRENT APPLICATION NUMBER: US/09/481,282
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 5247
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-481-282-20

Query Match 36.6%; Score 1586.2; DB 3; Length 5247;
Best Local Similarity 96.0%; Pred. No. 2.8e-258;
Matches 1656; Conservative 0; Mismatches 23; Indels 46; Gaps 1;

Qy 2608 CATGTGAGCAAAAGCCAGCAAAAGCCAGAGAACCGTAAAAAGGCGCGCTTCTGCGGTT 2667
Db 1250 CATGTGAGCAAAAGCCAGCAAAAGCCAGAGAACCGTAAAAAGGCGCGCTTCTGCGGTT 1309
Qy 2668 TTTTCATAGGCTCCGCCCTTCGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTG 2727
Db 1310 TTTTCATAGGCTCCGCCCTTCGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTG 1369
Qy 2728 GCGAAACCCGACAGACTATAAGATACAGAGCTTCCCTCCCTGGAAGCTCCCTCGTGG 2787
Db 1370 GCGAAACCCGACAGACTATAAGATACAGAGCTTCCCTCCCTGGAAGCTCCCTCGTGG 1429
Qy 2788 CTCTCTGTTCCGAGCCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCTTCGGAAG 2847

```
Db 1430 CTCTCTGTTCCGACCTTCCGCGCTTACCGGATACCTGTCCGCCCTTCTCCCTCCGGAAG 1489
Qy 2848 CGTGGCGCTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGCTGTAGGTTCGCTC 2907
Db 1490 CGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGCTGTAGGTTCGCTC 1549
Qy 2908 CAAGCTGGGCTGTGTGACGAAACCCCGGTTTCAGCCCGACCGCTTCGCTTCATCCGGTAA 2967
Db 1550 CAAGCTGGGCTGTGTGACGAAACCCCGGTTTCAGCCCGACCGCTTCGCTTCATCCGGTAA 1609
Qy 2968 CTATCGCTTTCAGTTCACACCCGCTTAAGACACGATTCATCGCCACTGGCAGCAGCCTGG 3027
Db 1610 CTATCGCTTTCAGTTCACACCCGCTTAAGACACGATTCATCGCCACTGGCAGCAGCCTGG 1669
Qy 3028 TAACAGGATTAGCAGAGCGAGTATGTAGGCGGTGTACAGATTCCTTGAAGTGTGCGCC 3087
Db 1670 TAACAGGATTAGCAGAGCGAGTATGTAGGCGGTGTACAGATTCCTTGAAGTGTGCGCC 1729
Qy 3088 TAACAGGCTACACTAGAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTAC 3147
Db 1730 TAACAGGCTACACTAGAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTAC 1789
Qy 3148 CTTTCGGAAGAGCTTGGTAGCTCTTGATCCGGCAAAACAACCAACCCGCTGGTAGCGGTG 3207
Db 1790 CTTTCGGAAGAGCTTGGTAGCTCTTGATCCGGCAAAACAACCAACCCGCTGGTAGCGGTG 1849
Qy 3208 TTTTCTTTGTTGCAAGCAGCAGATTCGCGCAGAAAAAAGGATCTCAAGAGATCTCTT 3267
Db 1850 TTTTCTTTGTTGCAAGCAGCAGATTCGCGCAGAAAAAAGGATCTCAAGAGATCTCTT 1909
Qy 3268 GATCTTTCTACCGGGTCTGAGCTCAGTGTGAACGAAACCTCAGTTAAAGGATTTGGT 3327
Db 1910 GATCTTTCTACCGGGTCTGAGCTCAGTGTGAACGAAACCTCAGTTAAAGGATTTGGT 1969
Qy 3328 CATGAGCGGATACATATTTGAATGATTTAGAAAAATTAACAAATAGGGGTTCCGCGCAC 3387
Db 1970 CATGAGATTTACAAAAAGGATCTTCACTAGA----- 2001
Qy 3388 ATTTCCCGGAAAGTGCACCTGTATCGGTGTGAATACCGCACAGATCGTAAGGAGA 3447
Db 2002 -----TCCCTTTTACGGTGTGAATACCGCACAGATCGTAAGGAGA 2043
Qy 3448 AAATACCGCATCAGGAAATTTAGCGTTAATATTCAGAGAACTCCTGTCAAGAGGCGGA 3507
Db 2044 AAATACCGCATCAGGAAATTTAGCGTTAATATTCAGAGAACTCCTGTCAAGAGGCGGA 2103
Qy 3508 TAGAGGCGGATCGCTCGGATCGGAGCGGCGATACCGTAAGCACGAGAGCGGTCA 3567
Db 2104 TAGAGGCGGATCGCTCGGATCGGAGCGGCGATACCGTAAGCACGAGAGCGGTCA 2163
Qy 3568 GCCCATTCGCGCCCAAGCTCTTACGCAATATACGGGTAGCCACGCTATGTCTCTGATAG 3627
Db 2164 GCCCATTCGCGCCCAAGCTCTTACGCAATATACGGGTAGCCACGCTATGTCTCTGATAG 2223
Qy 3628 CGGTCCGCCCAACCCAGCCGCCCAAGTTCGATGAATCCAGAAAAAGCGGCCATTTTCCACC 3687
Db 2224 CGGTCCGCCCAACCCAGCCGCCCAAGTTCGATGAATCCAGAAAAAGCGGCCATTTTCCACC 2283
Qy 3688 ATGATATTTCGCGCAGAGGATCGCCATGGGTACGACGAGATCTCTCGCGCTGGGGATG 3747
Db 2284 ATGATATTTCGCGCAGAGGATCGCCATGGGTACGACGAGATCTCTCGCGCTGGGGATG 2343
Qy 3748 CTGCGCTTTCAGCTTGGCGCAAGTTCGCTTGGCGGAGCCCTGATGCTCTTCTGTCAGA 3807
Db 2344 CTGCGCTTTCAGCTTGGCGCAAGTTCGCTTGGCGGAGCCCTGATGCTCTTCTGTCAGA 2403
Qy 3808 TCATCTTCATCGAACAAGCCGGCTTCCATCCGAGTACGTCTCGCTCGATGCGATGTTTC 3867
Db 2404 TCATCTTCATCGAACAAGCCGGCTTCCATCCGAGTACGTCTCGCTCGATGCGATGTTTC 2463
Qy 3868 GCTTGGTGTGCAATGGGAGGATAGCCGATCAAGCGTATGACCGCGCCGATTCATCA 3927
```

```
Db 2464 GCTTGGTGTGCAATGGGAGGTAGCCGATCAAGCGTATGACGCCCGCATTTGCATCA 2523
Qy 3928 GCCATGATGATATCTTCTCGGAGGAGCAAGGTGAGATGACAGGAGATCTCTGCCCGGC 3987
Db 2524 GCCATGATGATATCTTCTCGGAGGAGCAAGGTGAGATGACAGGAGATCTCTGCCCGGC 2583
Qy 3988 ACTTCGCCCAATAGCAGCAGTCCCTTCCCGCTTTCAGTGACAAAGTTCGAGCAGAGTGG 4047
Db 2584 ACTTCGCCCAATAGCAGCAGTCCCTTCCCGCTTTCAGTGACAAAGTTCGAGCAGAGTGG 2643
Qy 4048 CAAGGAAGCCCGCTGTGGCCAGCAGATAGCGCGCTGCTCTTTCAGTTCATTC 4107
Db 2644 CAAGGAAGCCCGCTGTGGCCAGCAGATAGCGCGCTGCTCTTTCAGTTCATTC 2703
Qy 4108 AGGSCACCGCAGCAGGTGCTTTCAGAAAAAGAACCGGGCGCCCTGCGCTGACAGCGG 4167
Db 2704 AGGSCACCGCAGCAGGTGCTTTCAGAAAAAGAACCGGGCGCCCTGCGCTGACAGCGG 2763
Qy 4168 AACACGCGCGCATCAGAGCAGCGGATTTGTCTGTGTCGCCAGTCATAGCCGAATAGCCTC 4227
Db 2764 AACACGCGCGCATCAGAGCAGCGGATTTGTCTGTGTCGCCAGTCATAGCCGAATAGCCTC 2823
Qy 4228 TCACACCAAGCGCGGAGAACCTGCGTGCAATCCATCTTTGTTCAATCATGCGGAAAGAT 4287
Db 2824 TCACACCAAGCGCGGAGAACCTGCGTGCAATCCATCTTTGTTCAATCATGCGGAAAGAT 2883
Qy 4288 CCTCATCTCTCTTTCATGATCAGAGCTTTGATCCCTCGCCATCAG 4332
Db 2884 CCTCATCTCTCTTTCATGATCAGAGCTTTGATCCCTCGCCATCAG 2928
```

Search completed: March 15, 2006, 04:59:37
Job time : 1306 secs

QY 2401 CGCTTTCCAGTCGGGAAACCTGTCTGTCAGCTCAATTAATGAATCGGCCAAACGCGCGG 2460
DB 2401 CGCTTTCCAGTCGGGAAACCTGTCTGTCAGCTCAATTAATGAATCGGCCAAACGCGCGG 2460
QY 2461 GAGAGCGGTTTGGGTAATGGGCGCTCTTGGCGCTCTGCTCTACTGCTGCTGCTGCTC 2520
DB 2461 GAGAGCGGTTTGGGTAATGGGCGCTCTTGGCGCTCTGCTCTACTGCTGCTGCTGCTC 2520
QY 2521 GGTCTTCCGTCGGCGAGCGGTATCAGCTCACTCAAAAGCGGTATACGTTATCCAC 2580
DB 2521 GGTCTTCCGTCGGCGAGCGGTATCAGCTCACTCAAAAGCGGTATACGTTATCCAC 2580
QY 2581 AGAATCAGGGGATTAACAGCAAGAAACATGTGAGCAAAAGGCGCAGCAAAAGGCGAGAA 2640
DB 2581 AGAATCAGGGGATTAACAGCAAGAAACATGTGAGCAAAAGGCGCAGCAAAAGGCGAGAA 2640
QY 2641 CCGTAAAAAGGCGCGTTGCTGGCGTTTTCATAGGCTCGGCCCTCCCTGACGAGATCA 2700
DB 2641 CCGTAAAAAGGCGCGTTGCTGGCGTTTTCATAGGCTCGGCCCTCCCTGACGAGATCA 2700
QY 2701 CAATAATCGAGCTCCCTCGTGGCTCTCTCTGTTCCGACCCCTGCGCTTACCGGATA 2760
DB 2701 CAATAATCGAGCTCCCTCGTGGCTCTCTCTGTTCCGACCCCTGCGCTTACCGGATA 2760
QY 2761 GTTTCCTCCCTGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCCCTGCGCTTACCGGATA 2820
DB 2761 GTTTCCTCCCTGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCCCTGCGCTTACCGGATA 2820
QY 2821 CTTGTCGCGCTTCTCCCTTGGGAGCGTGGCGCTTCTCAATGCTCAAGCTGATAGGTA 2880
DB 2821 CTTGTCGCGCTTCTCCCTTGGGAGCGTGGCGCTTCTCAATGCTCAAGCTGATAGGTA 2880
QY 2881 TCTCAGTTCGCTGATGCTGCTCAAGCTGGGCTGTGTCAGCAACCCCGGTTCA 2940
DB 2881 TCTCAGTTCGCTGATGCTGCTCAAGCTGGGCTGTGTCAGCAACCCCGGTTCA 2940
QY 2941 GCCCGACCGCTGCGCTTATCCGCTAACTATCGCTTTGAGTCCAAACCCGCTAAGACACGA 3000
DB 2941 GCCCGACCGCTGCGCTTATCCGCTAACTATCGCTTTGAGTCCAAACCCGCTAAGACACGA 3000
QY 3001 CTTATCGCCACTGCGCAGCAGCTGTAACAGGATTAAGCAGCGAGGTATGAGCGG 3060
DB 3001 CTTATCGCCACTGCGCAGCAGCTGTAACAGGATTAAGCAGCGAGGTATGAGCGG 3060
QY 3061 TGCTACAGAGTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGGACAGTATTGG 3120
DB 3061 TGCTACAGAGTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGGACAGTATTGG 3120
QY 3121 TATCTGCGCTCTGCTGAAGCCAGTTACTTTGGAAGAAAGAGTTGGTAGCTCTTTGATCCGG 3180
DB 3121 TATCTGCGCTCTGCTGAAGCCAGTTACTTTGGAAGAAAGAGTTGGTAGCTCTTTGATCCGG 3180
QY 3181 CAAACAAACACCGCTGATAGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 3240
DB 3181 CAAACAAACACCGCTGATAGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 3240
QY 3241 AAAAAAAGGATCTCAAGAGATCTTTGATCTTTTACCGGGTCTGACGCTCAGTGGAA 3300
DB 3241 AAAAAAAGGATCTCAAGAGATCTTTGATCTTTTACCGGGTCTGACGCTCAGTGGAA 3300
QY 3301 CGAAACTCAGTTAAGGATTTTGGTCAAGCGGATACATATTTGAAATGATTTAGAA 3360
DB 3301 CGAAACTCAGTTAAGGATTTTGGTCAAGCGGATACATATTTGAAATGATTTAGAA 3360
QY 3361 AAATAAACAATAGGGTTTCGGGCACATTTCCCGAAAGTCCACCTGTATGCGGTGT 3420
DB 3361 AAATAAACAATAGGGTTTCGGGCACATTTCCCGAAAGTCCACCTGTATGCGGTGT 3420
QY 3421 GAAATACCGCAGATCGTAAGAGAAATACCGCATCAGGAAATGTAAGCGTTAATA 3480
DB 3421 GAAATACCGCAGATCGTAAGAGAAATACCGCATCAGGAAATGTAAGCGTTAATA 3480

QY 3481 ATTCAAGAAATCGTCAAGAACGCGATAGAAGCGATGCGCTGCGAATCGGAGCGCG 3540
DB 3481 ATTCAAGAAATCGTCAAGAACGCGATAGAAGCGATGCGCTGCGAATCGGAGCGCG 3540
QY 3541 ATACCGTTAAAGACAGGAGAGCGGTCAAGCCATTTCGCGCAAGCTCTTCAGCAATATCA 3600
DB 3541 ATACCGTTAAAGACAGGAGAGCGGTCAAGCCATTTCGCGCAAGCTCTTCAGCAATATCA 3600
QY 3601 CCGGTAGCAAAACCTATGCTGATAGCGGTGCGCACACCCAGCGCGGCACAGTCCGATG 3660
DB 3601 CCGGTAGCAAAACCTATGCTGATAGCGGTGCGCACACCCAGCGCGGCACAGTCCGATG 3660
QY 3661 AATCCAGAAAGCGCCATTTCACCATGATATTTCGCAAGCAGGATCGCATGCGGTCT 3720
DB 3661 AATCCAGAAAGCGCCATTTCACCATGATATTTCGCAAGCAGGATCGCATGCGGTCT 3720
QY 3721 ACAGCAGATCTTCGCGCTGCGGATGCTGCTTGAAGCTGCGCAACAGTTTCGCTGCGG 3780
DB 3721 ACAGCAGATCTTCGCGCTGCGGATGCTGCTTGAAGCTGCGCAACAGTTTCGCTGCGG 3780
QY 3781 GCGAGCCCTGATGCTTTCGTCAGATCATCTGATCGAAGACCGGCTTCCATCCGA 3840
DB 3781 GCGAGCCCTGATGCTTTCGTCAGATCATCTGATCGAAGACCGGCTTCCATCCGA 3840
QY 3841 GTACGTGCTGCTGCGATGCGATGTTTCGCTTGGTGGTTCGAATGGGAGGTAGCGGATCA 3900
DB 3841 GTACGTGCTGCTGCGATGCGATGTTTCGCTTGGTGGTTCGAATGGGAGGTAGCGGATCA 3900
QY 3901 AGGTTATGACGCGCGCATTTGATCAGCATGATGATGATGATGATGATGATGATGATG 3960
DB 3901 AGGTTATGACGCGCGCATTTGATCAGCATGATGATGATGATGATGATGATGATGATG 3960
QY 3961 TGAGATGACAGGAGATCTTCCCGCGCATTTCCCGCAATAGCAGCCAGTCCCTTCCCGCT 4020
DB 3961 TGAGATGACAGGAGATCTTCCCGCGCATTTCCCGCAATAGCAGCCAGTCCCTTCCCGCT 4020
QY 4021 TCAGTCAACACGTCGAGCAGCTGCGCAAGAACCGCTGCTGGCAGCAGCATAGC 4080
DB 4021 TCAGTCAACACGTCGAGCAGCTGCGCAAGAACCGCTGCTGGCAGCAGCATAGC 4080
QY 4081 CCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4140
DB 4081 CCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4140
QY 4141 ACCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4200
DB 4141 ACCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4200
QY 4201 TGTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4260
DB 4201 TGTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4260
QY 4261 CCATCTGTTCAATCATGGAACGATCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4320
DB 4261 CCATCTGTTCAATCATGGAACGATCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4320
QY 4321 CTGCGCCATCAG 4332
DB 4321 CTGCGCCATCAG 4332

RESULT 2

US-10-811-028A-2

; Sequence 2, Application US/10811028A
; Publication No. US20050043258A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michael
; APPLICANT: Chen, Yen-Ju
; APPLICANT: Gentric, Inc.
; TITLE OF INVENTION: Methods of Treating Xerostomia and Xerophthalmia
; FILE REFERENCE: 020714-002410US
; CURRENT APPLICATION NUMBER: US/10/811,028A
; CURRENT FILING DATE: 2004-03-25

```

; PRIOR APPLICATION NUMBER: US 60/458,793
; PRIOR FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4293
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pMB1-HAMmSOD
; OTHER INFORMATION: plasmid expression vector
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1940)
; OTHER INFORMATION: n = g, a, c or t
US-10-811-028A-2

Query Match      96.3%; Score 4170.6; DB 8; Length 4293;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 4254; Conservative 0; Mismatches 39; Indels 39; Gaps 2;

Qy      1  CGGTGCGGGCCTCTTCGGTATTACGCCAGCTGGCGAAGAGGGGATGTCTCAAGGGGAT 60
Db      1  CGGTGCGGGCCTCTTCGGTATTACGCCAGCTGGCGAAGAGGGGATGTCTCAAGGGGAT 60

Qy      61  TAAGTTGGGTAAACGCCAGGGTTTTCCCACTCAAGCGTTGTAACCGAGCCCAAGTGAAT 120
Db      61  TAAGTTGGGTAAACGCCAGGGTTTTCCCACTCAAGCGTTGTAACCGAGCCCAAGTGAAT 120

Qy      121  TGTATACGACTCACTATAGGCGAATTTGGGTACTGGCCACAGAGCTTGGGCCATTGCAT 180
Db      121  TGTATACGACTCACTATAGGCGAATTTGGGTACTGGCCACAGAGCTTGGGCCATTGCAT 180

Qy      181  ACGTTGTATCCATATCAATATGACATTTATATTTGCTCATGTCACCAATTAACCGCA 240
Db      181  ACGTTGTATCCATATCAATATGACATTTATATTTGCTCATGTCACCAATTAACCGCA 240

Qy      241  TGTGACATTGATTATGACTAGTTATTAAATAGTAATCAATTAACGGGTCAATTAGTTCA 300
Db      241  TGTGACATTGATTATGACTAGTTATTAAATAGTAATCAATTAACGGGTCAATTAGTTCA 300

Qy      301  AGCCCATATATGGAGTTCCGGTTACATACTTACGGTAAATGGCCCGCTGGCTGACCG 360
Db      301  AGCCCATATATGGAGTTCCGGTTACATACTTACGGTAAATGGCCCGCTGGCTGACCG 360

Qy      361  CCCAACGACCCCGCCCAATTGACGTCATATGACGTATGTTCCCATAGTAACGCCAATA 420
Db      361  CCCAACGACCCCGCCCAATTGACGTCATATGACGTATGTTCCCATAGTAACGCCAATA 420

Qy      421  GGGACTTTCCATTTGACGTCATATGGGTGAGTATTTACGGTAAATGCGCCACTTGGCAGTA 480
Db      421  GGGACTTTCCATTTGACGTCATATGGGTGAGTATTTACGGTAAATGCGCCACTTGGCAGTA 480

Qy      481  CATCAAGTGTATCATATGCCAGTACGCCCTATTGACGTCAATGACGTAAATGGGCC 540
Db      481  CATCAAGTGTATCATATGCCAGTACGCCCTATTGACGTCAATGACGTAAATGGGCC 540

Qy      541  GCCTGGCATTTATGCCAGTACATGACCTTATGCGGACTTTTCCCTACTTGGCAGTACATCTAC 600
Db      541  GCCTGGCATTTATGCCAGTACATGACCTTATGCGGACTTTTCCCTACTTGGCAGTACATCTAC 600

Qy      601  GTATTAGTATCGCTATTACATGATGATGCGGTTTGGCAGTACATCAATGGGGGTGA 660
Db      601  GTATTAGTATCGCTATTACATGATGATGCGGTTTGGCAGTACATCAATGGGGGTGA 660

Qy      661  TAGCGGTTTGTACTACGGGGATTTCCAGTCTCCACCCCATTTGACGTCAATGGGAGTTG 720
Db      661  TAGCGGTTTGTACTACGGGGATTTCCAGTCTCCACCCCATTTGACGTCAATGGGAGTTG 720

Qy      721  TTTTGGCACCAAAATCAACGGGACTTTTCCAAATGTGCTAAACCTTCGGCCCATTTGACG 780
Db      721  TTTTGGCACCAAAATCAACGGGACTTTTCCAAATGTGCTAAACCTTCGGCCCATTTGACG 780

```

```

781  CAAATGGGCGGTAGGTAGCGTGTACGGTGGGAGGCTCTATATAGCAGAGCTCGTTAGTGAAC 840
781  CAAATGGGCGGTAGGTAGCGTGTACGGTGGGAGGCTCTATATAGCAGAGCTCGTTAGTGAAC 840
841  CGTCAGATCCGCTGGAGACGCCATCCACGCTGTTTGGACCTCCATAGAACACACCGGGAC 900
841  CGTCAGATCCGCTGGAGACGCCATCCACGCTGTTTGGACCTCCATAGAACACACCGGGAC 900
901  CGATCCAGCCTGACTCTAGCTAGCTCTGAGTGTGGTGGTGGAGCCCTGGGCGAGTTGGT 960
901  CGATCCAGCCTGACTCTAGCTAGCTCTGAGTGTGGTGGTGGAGCCCTGGGCGAGTTGGT 960
961  ATCAAGGTTACAGACAGGTTTAAAGAGACCAATAGAAACTGGGCATGTGGAGACAGAGA 1020
961  ATCAAGGTTACAGACAGGTTTAAAGAGACCAATAGAAACTGGGCATGTGGAGACAGAGA 1020
1021  AGACTCTTGGGTTTCTGATAGGCACTGACTCTCTCTGCTCTATTTGGTCTATTTTCCACCC 1080
1021  AGACTCTTGGGTTTCTGATAGGCACTGACTCTCTCTGCTCTATTTGGTCTATTTTCCACCC 1080
1081  TTAGGCTGCTGGTCTGAGCCTTAGGAGATCTCTCGAGGTGACCGGTATCGATAAGCTTGAT 1140
1081  TTAGGCTGCTGGTCTGAGCCTTAGGAGATCTCTCGAGGTGACCGGTATCGATAAGCTTGAT 1140
1141  ATCGAATTCGGGCGGCGCAGGAGCGCATCTCGTGGCTGTGCTGGCTTCGSCACGGGCTT 1200
1141  AATTCCACCATGGCTTC-----TAGCCCTTATGACGTGCTGACTATGCCAGTTTAGG 1193
1201  CAGCAGATCGGCGGCATCAGCGGTAGCACACGACACTAGCAGCATGTTGAGCCGGCAGTG 1260
1194  AGGACTTCT-----ATGTTGAGCCGGCAGTG 1221
1261  TGGCGCACAGCAGCAGCTGGCTCCGGTTTGGGTTATCTGGGCTCAGGCGAAGAC 1320
1222  TGGCGCACAGCAGCAGCTGGCTCCGGTTTGGGTTATCTGGGCTCAGGCGAAGAC 1281
1321  AGCTTCCCGACCTGCCCTACGACTAGCGGCCCTGGACCTCATCATCAACCGCAGATC 1380
1282  AGCTTCCCGACCTGCCCTACGACTAGCGGCCCTGGACCTCATCATCAACCGCAGATC 1341
1381  ATGCACTGTCACCAAGCAGCAGCGGCCCTACGTGAAACAACCTGAAACCTCAACCG 1440
1342  ATGCACTGTCACCAAGCAGCAGCGGCCCTACGTGAAACAACCTGAAACCTCAACCG 1401
1441  GAGAAGTACAGAGGGGCTTGGCCCAAGGAGATGTTACAGCCAGATAGCTCTTCAGGCT 1500
1402  GAGAAGTACAGAGGGGCTTGGCCCAAGGAGATGTTACAGCCAGATAGCTCTTCAGGCT 1461
1501  GCCTGAAAGTTCAATGTTGGTGTGTCATATCAATCATAGCATTTTCTGACAAACCTCAGC 1560
1462  GCCTGAAAGTTCAATGTTGGTGTGTCATATCAATCATAGCATTTTCTGACAAACCTCAGC 1521
1561  CCTAACGCTGTGGAGAACCCAAAGGGGAGTTGCTGGAAGCCATCAAAACGTGACTTGGT 1620
1522  CCTAACGCTGTGGAGAACCCAAAGGGGAGTTGCTGGAAGCCATCAAAACGTGACTTGGT 1581
1621  TCCTTTGACAAGTTTAAAGSAGAGCTGACGCTGATCTGTTGGTGTCCAAGGCTCAGT 1680
1582  TCCTTTGACAAGTTTAAAGSAGAGCTGACGCTGATCTGTTGGTGTCCAAGGCTCAGT 1641
1681  TGGGTTGGCTTGGTTTCAATAAGGAACGGGACACTTACAAATTTGCTGTGCTCAAAAT 1740
1642  TGGGTTGGCTTGGTTTCAATAAGGAACGGGACACTTACAAATTTGCTGTGCTCAAAAT 1701
1741  CAGGATCCACTGCAAGGAACCAACAGCCCTTATTCACCTGCTGGGATGATGATGTGGGAG 1800
1702  CAGGATCCACTGCAAGGAACCAACAGCCCTTATTCACCTGCTGGGATGATGATGTGGGAG 1761
1801  CAGGCTTACTACTTCAATATAAATGTCAGGCTGATTAATCTAAAGCTATTTGGAT 1860
1762  CAGGCTTACTACTTCAATATAAATGTCAGGCTGATTAATCTAAAGCTATTTGGAT 1821
1861  GTAATCAACTGGGAGAAATGTAACTGAAAGATACATAGGCTTGCATAAAAGTAAACCCAGT 1920

```

1822 Db GTAATCACTGGGAGAAATGTAATCTGAAAGATACATGGCTTGCAAAAGTAAACACCAT 1881
1921 QY CGTTATGCTCGAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1980
1882 Db CGTTATGCTGGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1941
1981 QY AAAAAACGGAATTCCTCGACGCCGGGGATCCACTAGTTCTAGAGCGCGCCACCGCG 2040
1942 Db AAAAAACGGAATTCCTCGACGCCGGGGATCCACTAGTTCTAGAGCGCGCCACCGCG 2001
2041 QY GTGAGCTCACAACTAGAAATGCAATGCAAAAAAATGCTTTATTTGTAATTTGTAATG 2100
2002 Db GTGAGCTCACAACTAGAAATGCAATGCAAAAAAATGCTTTATTTGTAATTTGTAATG 2061
2101 QY TATTGCTTTATTTGTAACCAATTAAGCTGCAATTAACCAATTAACCAATTAACCAATTAACCAATTA 2160
2062 Db TATTGCTTTATTTGTAACCAATTAAGCTGCAATTAACCAATTAACCAATTAACCAATTAACCAATTA 2121
2161 QY TTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTTTAAAGCCACAGCTCCAGCTT 2220
2122 Db TTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTTTAAAGCCACAGCTCCAGCTT 2181
2221 QY TTGTTCCCTTTAGTAGGGTTAATTTTCGAGCTTTGGCGTAATCATGTCATAGCTGTTTCC 2280
2182 Db TTGTTCCCTTTAGTAGGGTTAATTTTCGAGCTTTGGCGTAATCATGTCATAGCTGTTTCC 2241
2281 QY TGTGTGAATTTGTTATCCGCTCAAAATTCACAAATTAACCAATTAACCAATTAACCAATTAACCAATTA 2340
2242 Db TGTGTGAATTTGTTATCCGCTCAAAATTCACAAATTAACCAATTAACCAATTAACCAATTAACCAATTA 2301
2341 QY TAAAGCTCGGGTGCCCTAATGAGTGAGCTAACTCAATTAATTTGCGTTGCGCTCACTGCC 2400
2302 Db TAAAGCTCGGGTGCCCTAATGAGTGAGCTAACTCAATTAATTTGCGTTGCGCTCACTGCC 2361
2401 QY CGCTTTCCAGTCGGGAAAACCTGTGTCGACAGCTGCAATTAATGAATTCGGCAACCGCGGG 2460
2362 Db CGCTTTCCAGTCGGGAAAACCTGTGTCGACAGCTGCAATTAATGAATTCGGCAACCGCGGG 2421
2461 QY GAGAGCGGTTTCGCTATTGGCGCTCTTCGCGCTTCTCGCTCACTCACTCGCTCGCTCGCTC 2520
2422 Db GAGAGCGGTTTCGCTATTGGCGCTCTTCGCGCTTCTCGCTCACTCACTCGCTCGCTCGCTC 2481
2521 QY GGTGCTTCGCTCGCGAGCGGTATCAGCTCACTCAAAAGCGGTAAATCGGTTATCCAC 2580
2482 Db GGTGCTTCGCTCGCGAGCGGTATCAGCTCACTCAAAAGCGGTAAATCGGTTATCCAC 2541
2581 QY AGAATCAGGGATAACGCGAGGAAAGACATGTGAGCAAAAGGCGGCAAAAGGCGGAA 2640
2542 Db AGAATCAGGGATAACGCGAGGAAAGACATGTGAGCAAAAGGCGGCAAAAGGCGGAA 2601
2641 QY CCGTAAAGGCGCGGTTGCTGCGCTTTTCCATAGCTCCGCGCCCTGACGAGCATCA 2700
2602 Db CCGTAAAGGCGCGGTTGCTGCGCTTTTCCATAGCTCCGCGCCCTGACGAGCATCA 2661
2701 QY CAAAAATCGAGCTCAAGTCAGAGGTGGGAAACCCGACAGGACTATAAGATACCAAGC 2760
2662 Db CAAAAATCGAGCTCAAGTCAGAGGTGGGAAACCCGACAGGACTATAAGATACCAAGC 2721
2761 QY GTTTCCCTCGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCTCGCGCTTACCGGATA 2820
2722 Db GTTTCCCTCGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCTCGCGCTTACCGGATA 2781
2821 QY CTGTGCGGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTCAAGCTGTAGGTA 2880
2782 Db CTGTGCGGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTCAAGCTGTAGGTA 2841
2881 QY TCTCAGTTCCGTTAGTGTGCTCCAGCTGGGCTGTGTGACGAAACCCCGCTTCA 2940
2842 Db TCTCAGTTCCGTTAGTGTGCTCCAGCTGGGCTGTGTGACGAAACCCCGCTTCA 2901
2941 QY GCCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCAACCCCGGTAAAGACGA 3000

2902 Db GCCCGACCGCTGCGCTTATTCGGTAACTATCGTCTTGAGTCCAAACCCGCTAAGACACGA 2961
3001 QY CTTTATCGCACTCGGAGCAGCCACTCGTAAACAGGATTAGCAGAGCAGGTTATGTAGCGG 3060
2962 Db CTTTATCGCACTCGGAGCAGCCACTCGTAAACAGGATTAGCAGAGCAGGTTATGTAGCGG 3021
3061 QY TGTACAGAGTTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAGGACAGTATTG 3120
3022 Db TGTACAGAGTTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAGGACAGTATTG 3081
3121 QY TATCTCGCTCTGCTGAAAGCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGAATCCG 3180
3082 Db TATCTCGCTCTGCTGAAAGCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGAATCCG 3141
3181 QY CAAACAAACACCGCTGGTAGCGGTGTTTTTTGTTGCAAGCAGCAGATTACGCGCAG 3240
3142 Db CAAACAAACACCGCTGGTAGCGGTGTTTTTTGTTGCAAGCAGCAGATTACGCGCAG 3201
3241 QY AAAAAAAGGATCTCAAGAAAGATCCTTTTGATCTTTTCTACGGGCTCTGACGCTCAGTGGAA 3300
3202 Db AAAAAAAGGATCTCAAGAAAGATCCTTTTGATCTTTTCTACGGGCTCTGACGCTCAGTGGAA 3261
3301 QY CGAAAACTCAGCTTAAAGGATTTTGTCTATGAGCGGATACATATTTGAATGTATTAGAA 3360
3262 Db CGAAAACTCAGCTTAAAGGATTTTGTCTATGAGCGGATACATATTTGAATGTATTAGAA 3321
3361 QY AATAAACAATAAGGGTTCCCGCAGCATTTCCCGAAAGTCCACCTGTATGCGGTGT 3420
3322 Db AATAAACAATAAGGGTTCCCGCAGCATTTCCCGAAAGTCCACCTGTATGCGGTGT 3381
3421 QY GAAATACCCGACAGATGCGTAAGGAGAAAAATACCGCATCAGGAAATTTGTAAGCGTTAATA 3480
3382 Db GAAATACCCGACAGATGCGTAAGGAGAAAAATACCGCATCAGGAAATTTGTAAGCGTTAATA 3441
3481 QY ATTCAAGAACTCTGTCAAAGAGCGGATAGAGGCGATGCGCTGCGAAATCGGAGCGGCG 3540
3442 Db ATTCAAGAACTCTGTCAAAGAGCGGATAGAGGCGGATGCGCTGCGAAATCGGAGCGGCG 3501
3541 QY ATACCGTAAAGCAGGAGGAGCGGTGAGCGCATTTCCCGCAAGCTCTTCAGCAATATCA 3600
3502 Db ATACCGTAAAGCAGGAGGAGCGGTGAGCGCATTTCCCGCAAGCTCTTCAGCAATATCA 3561
3601 QY CGGGTACCAACGCTATGCTCTGATAGCGGTGCGGCACACCCAGCGGCGCACAGTCCGATG 3660
3562 Db CGGGTACCAACGCTATGCTCTGATAGCGGTGCGGCACACCCAGCGGCGCACAGTCCGATG 3621
3661 QY AATCCGAAAGCGGCGCATTTTCCACCATGATATTCGGCAAGCAGGCGCATCGCCATGGTC 3720
3622 Db AATCCGAAAGCGGCGCATTTTCCACCATGATATTCGGCAAGCAGGCGCATCGCCATGGTC 3681
3721 QY ACGACGAGATCTCGCGCTCGGCGCATGCTCGCTGAGCTGCGCAACAGTTCCGCTGGC 3780
3682 Db ACGACGAGATCTCGCGCTCGGCGCATGCTCGCTGAGCTGCGCAACAGTTCCGCTGGC 3741
3781 QY GCGAGCCCCTGATGCTCTTTCGATCATCTGATCGAAGACCGGCTTCCATCCGA 3840
3742 Db GCGAGCCCCTGATGCTCTTTCGATCATCTGATCGAAGACCGGCTTCCATCCGA 3801
3841 QY GTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGTGCAATGGGCGAGTAGCGGATCA 3900
3802 Db GTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGTGCAATGGGCGAGTAGCGGATCA 3861
3901 QY AGCGTATGACGCGCGCGCATTCATCAGCATGATGATGATCTTCTCGGCGAGGCAAGG 3960
3862 Db AGCGTATGACGCGCGCGCATTCATCAGCATGATGATGATCTTCTCGGCGAGGCAAGG 3921
3961 QY TGAGATGACAGAGATCTTCGCCCCCGGCACTTCGCCCAATAGCAGCAGTCCCTTCCGCT 4020
3922 Db TGAGATGACAGAGATCTTCGCCCCCGGCACTTCGCCCAATAGCAGCAGTCCCTTCCGCT 3981
4021 QY TCAGTGACAACTCGAGCAGCTGCGCAAGGAAACCCCGCTCGTGGCGCAGCAGATAGC 4080
3982 Db TCAGTGACAACTCGAGCAGCTGCGCAAGGAAACCCCGCTCGTGGCGCAGCAGATAGC 4041

Qy	4081	CGCGCTGCCTCTCTTTCAGCTTCATTCAGGGCACCGGACAGGTCGGTCTTTGCACAAAAGA	4144
Db	4042	CGCGCTGCCTCTCTTTCAGCTTCATTCAGGGCACCGGACAGGTCGGTCTTTGCACAAAAGA	4101
Qy	4141	ACGGGGCGCCCCCTCGCGTGCAGCGGGAAACAACGGCGGCATCAGAGCAGCCGATTTGTCTGT	4200
Db	4102	ACGGGGCGCCCCCTCGCGTGCAGCGGGAAACAACGGCGGCATCAGAGCAGCCGATTTGTCTGT	4161
Qy	4201	TGTGCCAGTCATAGCCGGAATAGCCTCTCCACCAGCGCGCGGAGAACTCGTGGTGCAT	4260
Db	4162	TGTGCCAGTCATAGCCGGAATAGCCTCTCCACCAGCGCGCGGAGAACTCGTGGTGCAT	4221
Qy	4261	CCATCTTGTTCAATCATGCGAAACGATCCTCATCTCTGTCTCTTGATCAGAGCTTGATCCC	4320
Db	4222	CCATCTTGTTCAATCATGCGAAACGATCCTCATCTCTGTCTCTTGATCAGAGCTTGATCCC	4281
Qy	4321	CTGCGGCATCAG	4332
Db	4282	CTGCGGCATCAG	4293

```

RESULT 3
US-10-811-028A-6
; Sequence 6, Application US/10811028A
; Publication No. US20050043258A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michael
; APPLICANT: Chen, Yen-Ju
; APPLICANT: Generic, Inc.
; TITLE OF INVENTION: Methods of Treating Xerostomia and Xerophthalmia
; FILE REFERENCE: 020714-002410US
; CURRENT APPLICATION NUMBER: US/10/811,028A
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US 60/458,793
; PRIOR FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 4187
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:pMB1-EcSD
; OTHER INFORMATION: plasmid expression vector
US-10-811-028A-6

```

Query Match	74.9%;	Score 3245.6;	DB 8;	Length 4187;
Best Local Similarity	86.2%;	Pred. No. 0;		
Matches 3733;	Conservative	0;	Mismatches 454;	Indels 145; Gaps 7;
QY	1	CGGTGCGGCGCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGATGCTCTGCAAGGCCAT	60	
Db	1	CGGTGCGGCGCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGATGCTCTGCAAGGCCAT	60	
QY	61	TAAGTTGGGTAAAGCCAGGGTTTTCCAGTCACGACGTTGTAAACAGCGGCCAGTGAAT	120	
Db	61	TAAGTTGGGTAAAGCCAGGGTTTTCCAGTCACGACGTTGTAAACAGCGGCCAGTGAAT	120	
QY	121	TGTAATACGACTCACTATAGGGCGAATTTGGGTACTGGGCCACAGAGCTTTGGCCCCATTGCAT	180	
Db	121	TGTAATACGACTCACTATAGGGCGAATTTGGGTACTGGGCCACAGAGCTTTGGCCCCATTGCAT	180	
QY	181	ACGTTGTATCCATATCATAAATATGTACATTTATATTGGCTCATGTCCAAACATTACCGCCA	240	
Db	181	ACGTTGTATCCATATCATAAATATGTACATTTATATTGGCTCATGTCCAAACATTACCGCCA	240	
QY	241	TGTTGACATTGATTTACTAGTTTATTAAATAGTAATCAATTCACGGGGTCATTAGTTTCAT	300	
Db	241	TGTTGACATTGATTTACTAGTTTATTAAATAGTAATCAATTCACGGGGTCATTAGTTTCAT	300	
QY	301	AGCCCATATATGGAGCTTCGCGGCTTACATAACCTTACGGTAAATGGCCCGCGCTGGCTGACCG	360	

Db	301	AGCCCATATATGAGTTCGCGTTACATAACTTACGGTAAATGGCCCGCTGGCTGACCG	360
Qy	361	CCCAACGACCCCGCCCATTTGACGTCAATAATGACGTATGTTCCCATATGATAACGCCAATA	420
Db	361	CCCAAACGACCCCGCCCATTTGACGTCAATAATGACGTATGTTCCCATATGATAACGCCAATA	420
Qy	421	GGGACTTTCCATTTGACGTCAATGGGTGGAGTATTTACGGTAAATCTGCCACTTTGGCAGTA	480
Db	421	GGGACTTTCCATTTGACGTCAATGGGTGGAGTATTTACGGTAAATCTGCCACTTTGGCAGTA	480
Qy	481	CATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACAGGTAAATGGCCC	540
Db	481	CATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACAGGTAAATGGCCC	540
Qy	541	GCCTGGCAATATGCCCAAGTACATGACCTTATGGGACTTTCTTACTTTGGCAGTACATCTAC	600
Db	541	GCCTGGCAATATGCCCAAGTACATGACCTTATGGGACTTTCTTACTTTGGCAGTACATCTAC	600
Qy	601	GTATTAGTCATCGCTATTACCATGTTGATGCGGTTTTGGCAGTACATCAATGGGCGTGA	660
Db	601	GTATTAGTCATCGCTATTACCATGTTGATGCGGTTTTGGCAGTACATCAATGGGCGTGA	660
Qy	661	TAGCGGTTTGACTCAGCGGATTTCCAAGTCTCCACCCCATTCACGTCAATGGGAGTTTG	720
Db	661	TAGCGGTTTGACTCAGCGGATTTCCAAGTCTCCACCCCATTCACGTCAATGGGAGTTTG	720
Qy	721	TTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCCCCATTTGACG	780
Db	721	TTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCCCCATTTGACG	780
Qy	781	CAAAATGGCGGTAGCGGTGTACGGTGGGAGTCTATATAGCAGAGCTCGTTAGTGAAC	840
Db	781	CAAAATGGCGGTAGCGGTGTACGGTGGGAGTCTATATAGCAGAGCTCGTTAGTGAAC	840
Qy	841	CGTCAGATCGCTGGAGACGCCATTCACGCTGTTTGGACCTCCATAGAACACCCGGAC	900
Db	841	CGTCAGATCGCTGGAGACGCCATTCACGCTGTTTGGACCTCCATAGAACACCCGGAC	900
Qy	901	CGATCCAGCCTGACTCTAGCCTAGCTCTGAAGTTGGTGGTGGCGCCCTGGCGCAGGTTGGT	960
Db	901	CGATCCAGCCTGACTCTAGCCTAGCTCTGAAGTTGGTGGTGGCGCCCTGGCGCAGGTTGGT	960
Qy	961	ATCAAGGTTTACAGACAGGTTTAAAGAGACCAATAGAAAATCGGCGATGTGGAGACAGAGA	1020
Db	961	ATCAAGGTTTACAGACAGGTTTAAAGAGACCAATAGAAAATCGGCGATGTGGAGACAGAGA	1020
Qy	1021	AGACTCTGGGTTTCTCATAGGCACTGACTCTCTCTGCTATTGGTCTATTTTCCCAACC	1080
Db	1021	AGACTCTGGGTTTCTCATAGGCACTGACTCTCTCTGCTATTGGTCTATTTTCCCAACC	1080
Qy	1081	TTAGGCTGCTGCTGAGCCTTAGGAGATCTCTCGAGTTCGACCGGTATCGATAAGCTTGTAT	1140
Db	1081	TTAGGCTGCTGCTGAGCCTTAGGAGATCTCTCGAGTTCGACCGGTATCGATAAGCTTGTAT	1140
Qy	1141	ATCGAATTCGGGGCGCGCAGGACGCACTCGTGGCTGTGGTGGCTTCGGCAGCGGCTT	1200
Db	1141	TGGCAGCCGGTGCCTTCGACGCCCTTGGACGGCGGAGACTCGGCGGAGGCCAACTCTGACT	1200
Qy	1201	CAGCAGATTCGCGGCATCAGCGGTAGCACACAGCACTAGCAGCATGTTTCAGCGCGGCACTG	1260
Db	1201	CGGCGGATGGATCCGAGACATGTACGCCAAGGTACGGAGATCTGGCAGGAGTCTATGC	1260
Qy	1261	TGCGGCACACGAGCGAGCTGGCTCCGGTTTTGGGGTATCTGGGCTCCAGGCAGAACGAC	1320
Db	1261	AGCGCGGGAGGACGACAGGCAACGCTTCCAGCGGCTTCGAGGTCAGCCGCTCGGCCACGC	1320
Qy	1321	AGCCTCCCGACCTGCCCTCTAGCACTACGGCGCCCTGGAACTCTCACATCAACGCGCAGATC	1380
Db	1321	TGGA- GCGCGGCAACCCCGGGTGACCGCGCTCGTCTCTTCCGGCAGCTTTCGCCCGC	1379
Qy	1381	ATGCACTGCAACCAAGCAAGCAACGCGCGCCTTACGTGAACAACTTGAACGTCAACGAG	1440
Db	1380	GCCAACTCGACGCTTCTTCGCGCTCGAGGGCTTCCGACCGAGCGCAACAGTCTCC-AG	1438

Qy 1441 GAGAAAGTACAGGAGCGTGGCCAAAGGAGATGTACAGCCAGATAGCTCTTACGCT 1500
 Db 1439 CCGGCCATCCACGTGACACAGTTCGGGACCTGAGCAGGGCTGCGAGTCCACCGGGC 1498
 Qy 1501 GCATGAAGTTCAATGGTGGTGTATATCAATCATAGCATTTTCTGGACAAACCTCAGC 1560
 Db 1499 CCATCAACACCGCTGGCG-----TGCCGACCCCGCAGC 1533
 Qy 1561 CCTAACGCTGTGGAGAACCCAAAGGGAGTTGCTGGAAGCATCAAACTGACTTTGGT 1620
 Db 1534 ACCCGGGGACTTCGGCAACTTCGGGTTCGGGACGGAGCTCTGGAGGTACCGCGCG 1593
 Qy 1621 TCTTTGACAAAGTTTAAAGGAAAGCTGACGGCTGCATCTGTGTGTCTCAAGGCTCAGGT 1680
 Db 1594 GCCT-----GGCGGCTCGCTCGCGGCGCGCACTCCATC 1628
 Qy 1681 TGGGGTGGCTGTGTTTCAATAAGAAAGGAGCACTTACAAATGTGCTGTGTTCCAAAT 1740
 Db 1629 GTGGCGGGCGC-----TGGTCTCCAGCTGGGAGGACGACCTGGCGCGCG 1678
 Qy 1741 CAGGATCCACTGCAAGGAACAACAGGCTTATTCACCTGCTGGGGATTGATGTGGGAG 1800
 Db 1679 CGGCAACAGGCGAGCTGGAGAACG-----GGAACGGCGCGC 1717
 Qy 1801 CACGCTTACTACCTTCAAGTATAAAATGTTCAGGCTGATTTATCTAAAGCTATTGGAAAT 1860
 Db 1718 CGGCTGGCTGCTGCTGCTGGTGGCGCTGTCGGGCGCGGCTCTGGGAGCGCCAGCGCG 1777
 Qy 1861 GTAATCAACTGGGAGATGTAACTGAAGATACATGCTTGAAGTAAACACAGAT 1920
 Db 1778 GGAGCACTCAGAGCGCAAGAGCGCGCGCGGAGGAGTGCAGGCGCGCTGAAAGCT 1837
 Qy 1921 CGTTATCTGCAAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
 Db 1838 TGATATCG----- 1845
 Qy 1981 AAAAAACGGAATTCCTGACGCGGGGGATCCACTAGTTCTAGAGCGCGCGCCAGCGCG 2040
 Db 1846 -----AATTCCTGACGCGGGGATCCACTAGTTCTAGAGCGCGCGCCAGCGCG 1995
 Qy 2041 GTGAGCTCACAACTAGATGCAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 2100
 Db 1896 GTGAGCTCACAACTAGATGCAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1955
 Qy 2101 TATGCTTTATTTGTAACCATTAAGCTCAATTAAGCTCAATTAAGCTCAATTAAGCTCAAT 2160
 Db 1956 TATGCTTTATTTGTAACCATTAAGCTCAATTAAGCTCAATTAAGCTCAATTAAGCTCAAT 2015
 Qy 2161 TTTTATGTTTTCAGGTTTCAGGAGGAGTGTGGGAGGTTTTTAAAGCCACAGCTCCAGCTT 2220
 Db 2016 TTTTATGTTTTCAGGTTTCAGGAGGAGTGTGGGAGGTTTTTAAAGCCACAGCTCCAGCTT 2075
 Qy 2221 TTGTTCCCTTTAGTGGGTTAATTCAGCTTGGCGTAAATCATGTTGATGTTTTC 2280
 Db 2076 TTGTTCCCTTTAGTGGGTTAATTCAGCTTGGCGTAAATCATGTTGATGTTTTC 2135
 Qy 2281 TGTGTGAATTTGTTATCCGCTCAAAATTCACACAAATACAGAGCGGAGGAGGAGGAGGAG 2340
 Db 2136 TGTGTGAATTTGTTATCCGCTCAAAATTCACACAAATACAGAGCGGAGGAGGAGGAGGAG 2195
 Qy 2341 TAAAGCTCGGGTGCCTTAATGAGTGAGTAACTCAATTAATTTGCGTTGGCTCACTGCC 2400
 Db 2196 TAAAGCTCGGGTGCCTTAATGAGTGAGTAACTCAATTAATTTGCGTTGGCTCACTGCC 2255
 Qy 2401 CGCTTTCAGTCCGGAACCTGTCGCGAGCTGATTAATTAATTAATTAATTAATTAATTAAT 2460
 Db 2256 CGCTTTCAGTCCGGAACCTGTCGCGAGCTGATTAATTAATTAATTAATTAATTAATTAAT 2315
 Qy 2461 GAGAGCGGTTTGGGTTTGGGCGCTCTTCGCTTCTGCTCACTGACTCGTGGCTC 2520
 Db 2316 GAGAGCGGTTTGGGTTTGGGCGCTCTTCGCTTCTGCTCACTGACTCGTGGCTC 2375

Qy 2521 GGTCTGCTGGCTGCGGAGCGGTATCAGCTCACTCAAGGCGGTAAATACGTTTATCCAC 2580
 Db 2376 GGTCTGCTGGCTGCGGAGCGGTATCAGCTCACTCAAGGCGGTAAATACGTTTATCCAC 2435
 Qy 2581 AGAATCAGGGGATAAACGAGGAAAGAAATGTGAGGAAAGGCGGAGGCGGAGGCGGAGG 2640
 Db 2436 AGAATCAGGGGATAAACGAGGAAAGAAATGTGAGGAAAGGCGGAGGCGGAGGCGGAGG 2495
 Qy 2641 CCGTAAAGGAGCGCGGTGCTGGCTTTTCCATAGGCTCGGCGGCTGACGAGGATCA 2700
 Db 2496 CCGTAAAGGAGCGCGGTGCTGGCTTTTCCATAGGCTCGGCGGCTGACGAGGATCA 2555
 Qy 2701 CAAAAATCGACGCTCAAGTCAGAGGTGGGAAACCCGACAGGACTATAAGATACACAGG 2760
 Db 2556 CAAAAATCGACGCTCAAGTCAGAGGTGGGAAACCCGACAGGACTATAAGATACACAGG 2615
 Qy 2761 GTTTCCGCTTGGAGGCTCCCTCGTGGCTCTCTGTTCCGACCTCGGCTTACCGGATA 2820
 Db 2616 GTTTCCGCTTGGAGGCTCCCTCGTGGCTCTCTGTTCCGACCTCGGCTTACCGGATA 2675
 Qy 2821 CCTGTCCGCTTCTCCCTTCGGGAAAGCGTGGCGCTTTCTCAATGCTCAGCTGTAGGTA 2880
 Db 2676 CCTGTCCGCTTCTCCCTTCGGGAAAGCGTGGCGCTTTCTCAATGCTCAGCTGTAGGTA 2735
 Qy 2881 TCTCAGTTCCGCTGTAGTCTGCTCCAAAGCTGGGCTGTGTGCAGAAACCCCGCTTCA 2940
 Db 2736 TCTCAGTTCCGCTGTAGTCTGCTCCAAAGCTGGGCTGTGTGCAGAAACCCCGCTTCA 2795
 Qy 2941 GCGCGAGCTGCGCTTATCCGCTTAACTATGCTTGTAGTCCAAACCCCGTAAAGACAG 3000
 Db 2796 GCGCGAGCTGCGCTTATCCGCTTAACTATGCTTGTAGTCCAAACCCCGTAAAGACAG 2855
 Qy 3001 CTTTATCGCACTGCGAGCAGCTGCTAACAGATTTAGCAGAGGAGTGTAGGCGG 3060
 Db 2856 CTTTATCGCACTGCGAGCAGCTGCTAACAGATTTAGCAGAGGAGTGTAGGCGG 2915
 Qy 3061 TGCTACAGAGTTCTTGAAGTGGTGGCTTAACTACGGCTACACTAGAAAGGACAGTATTGG 3120
 Db 2916 TGCTACAGAGTTCTTGAAGTGGTGGCTTAACTACGGCTACACTAGAAAGGACAGTATTGG 2975
 Qy 3121 TATCTGGCTCTGCTGAGGCGAGTACCTTCGGAAAGAGGTTGGTAGCTCTTGTATCCGG 3180
 Db 2976 TATCTGGCTCTGCTGAGGCGAGTACCTTCGGAAAGAGGTTGGTAGCTCTTGTATCCGG 3035
 Qy 3181 CAAACAAACACCGCTGCTGAGCGGTGTTTTTGTGCAAGCAGCAGATTTACCGCAG 3240
 Db 3036 CAAACAAACACCGCTGCTGAGCGGTGTTTTTGTGCAAGCAGCAGATTTACCGCAG 3095
 Qy 3241 AAAAAAGGATCTCAAGAGATCCTTTGATCTTTTCTACGGGCTCTGACGCTCAGTGGAA 3300
 Db 3096 AAAAAAGGATCTCAAGAGATCCTTTGATCTTTTCTACGGGCTCTGACGCTCAGTGGAA 3155
 Qy 3301 CGAAACTCAGTTAAGGATTTTGTGTCAGCGGATACATATTTGAATGTTATTAGAA 3360
 Db 3156 CGAAACTCAGTTAAGGATTTTGTGTCAGCGGATACATATTTGAATGTTATTAGAA 3215
 Qy 3361 AATAAAACAAATAGGAGTTCGCGCAGATTTCCCGAAAGTGCACCTGTATGCGGTGT 3420
 Db 3216 AATAAAACAAATAGGAGTTCGCGCAGATTTCCCGAAAGTGCACCTGTATGCGGTGT 3275
 Qy 3421 GAAATACCGCAGATGCTGAGGAGAAATACCGCATCAGGAAATTTGTAAGCGTTAATA 3480
 Db 3276 GAAATACCGCAGATGCTGAGGAGAAATACCGCATCAGGAAATTTGTAAGCGTTAATA 3335
 Qy 3481 ATTCAAGAACTCCTCAAGAGCGGATGAGGCGATGCGGATCGGATCGGAGCGGCG 3540
 Db 3336 ATTCAAGAACTCCTCAAGAGCGGATGAGGCGATGCGGATCGGATCGGAGCGGCG 3395
 Qy 3541 ATACCGTAAAGCAGGAGGAGCGGTCAAGCGGATTTGCGCGCAAGCTCTTCAGCAATATCA 3600
 Db 3396 ATACCGTAAAGCAGGAGGAGCGGTCAAGCGGATTTGCGCGCAAGCTCTTCAGCAATATCA 3455
 Qy 3601 CGGGTAGCCAAACGCTATGCTCTGATAGCGGTTCGCCACACCCAGCGCGGCGCATG 3660

Db 961 ATCAAGGTTAACAAGAGGTTAAGGAGACCAATAGAAATCGGGCATGTGGAGACAGAGA 1020
Qy 1021 AGACTCTTGGTCTTCTGATAGGCACTGACTCTCTCTGCTTATTTGGTCTATTTCCACCC 1080
Db 1021 AGACTCTTGGTCTTCTGATAGGCACTGACTCTCTCTGCTTATTTGGTCTATTTCCACCC 1080
Qy 1081 TTAGGCTGCTGGTCTGAGCCTTAGAGATCTCTCGAGGTGCAACGGTATCGATAGCTTGAT 1140
Db 1081 TTAGGCTGCTGGTCTGAGCCTTAGAGATCTCTCGAGGTGCAACGGTATCGATAGCTTGAT 1140
Qy 1141 ATCGAATTCGGGGCGGCGAGGAGCGGCACTGCTGGTCTGCTGGTCTGCGAGCGGCTT 1200
Db 1141 ATCAGAGAGACCATGGCTTGACCTTTGCTTTACTGGTGGGCCCTCTCTGGTGC----- 1195
Qy 1201 CAGCAGATCGCGGCATCAGCGGTAGCACAGCAGCACTAGCAGCATGTTGACCGCGGAGTG 1260
Db 1196 -----TCAGCTGCAAGTCAAGCTGCTCTGTTGGGCTGATCTG 1233
Qy 1261 TGGCGCACAGCAGCAGCTGGCTCCGGTTTGGGGTATCTGGGCTCCAGCGCAGAGCAC 1320
Db 1234 CCTCAAAACCCACAG-----CCTGGGTAGCAGGAGACCTTG 1269
Qy 1321 AGCTCTCCGACCTGCCCTAGGACTACGGCGCCCTGGAACTCATCAACGCGCAGATC 1380
Db 1270 ATGCTCTCGCACAG-----ATCAGGAGAAATC 1296
Qy 1381 ATGCAGCTGCACACAGCAGCACCACCGCGCTACGTGAAACACCTGAAGCTCACCGAG 1440
Db 1297 TCTCTTTCTCTGCTTTGAAGGACAGACATGATCTTGGATTTCCCGAGGAGATTTGGC 1356
Qy 1441 GAGAAGTACCAGGAGCGGTTGGCCAAAGGAGATGTTACAGCCACAGATAGCTTTCAGCCT 1500
Db 1357 AACGAGTTCCAAAGGCTGAACCA----- 1381
Qy 1501 GCAGTGAAGTTCAATGGTGGTGTGTCATATCAATCATAGCATTTTCTGGACAAACCTCAGC 1560
Db 1382 -----TCCCTGTCTCCATGAGATGATCCAGCAGATCTTCAAT 1419
Qy 1561 CCTAAGCGGTGGAGAACCCAAAGGGAGTGTCTGGAAGCCATCAACGTGATTTGGT 1620
Db 1420 CTCTTCAAGCAAAAGHACTATCTGCTGTTGGATGAGACCTCTCTAGACAAATTTCTAC 1479
Qy 1621 TCTTTTGACAAGTTTAAAGGAAAGCTGACCGCTGTCATCTGTGTGTGTCGAAGGCTCAGGT 1680
Db 1480 ACTGAACTCTACAGCAGCTGAATGACCTGGAAGCCTGTGT-----GATACAGGGGT 1532
Qy 1681 TGGGTTGGCTTGTGTTCAATAGGAACGGGGACACTTAACAAATGCTGCTGTTGCCAAT 1740
Db 1533 GGGGGTGACAGAGACTCCCTGTATGAAGGAGGACTC----- 1568
Qy 1741 CAGGATCCACTGCAAGGAACAAAGGCGCTTATTCCTGCTGGGGATTGATGTGGGAG 1800
Db 1569 -----CATTTGCTGTGAGGAATACTTCCAAAGA 1599
Qy 1801 CAGCTTTACTACCTTCAAGTAAATAAATGTGAGGCTGATTTCTAAAGCTATTTGGAAAT 1860
Db 1600 ATCACTCTCTATCTGAAAGAGAAATAACAGCCCTTGTGCTGGGAGTTGTACAGACA 1659
Qy 1861 GTAATCACTGGGGAGATGTAATCTGAAGATACATGGCTTGCNAAGATTAACACAGAT 1920
Db 1660 GAAATCA-----TGAGAT 1672
Qy 1921 CGTTATCTCGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1980
Db 1673 CTTTTCTTTCTTCAACAACTTGCAGAAAGTTTGAAGATAGGAATGAATACTGGTTC 1732
Qy 1981 AAAAAACGAAATTCCTGACCGCGGGGATCCACTAGTTCTAGAGCGGCGCCACCGCG 2040
Db 1733 AA-----CATGGAATGAGCTAGAGCGGCGCCACCGCG 1766
Qy 2041 GTGAGCTCCAACTAGATGAGTGAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2100

Db 1767 GTGAGCTCCACAACTAGAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 1836
Qy 2101 TATTGCTTTATTTGTAACCAATTAAGCTGCAATTAAGCTGCAATTAAGCTGCAATTAAGCT 2160
Db 1827 TATTGCTTTATTTGTAACCAATTAAGCTGCAATTAAGCTGCAATTAAGCTGCAATTAAGCT 1886
Qy 2161 TTTTATGTTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCCACAGCTCCAGCTT 2220
Db 1887 TTTTATGTTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCCACAGCTCCAGCTT 1946
Qy 2221 TTGTTCCCTTTAGTAGGGTTAAATTCGAGCTTGGCGTAAATCATGCTGCTAGCTGTTTCC 2280
Db 1947 TTGTTCCCTTTAGTAGGGTTAAATTCGAGCTTGGCGTAAATCATGCTGCTAGCTGTTTCC 2006
Qy 2281 TGTGTGAAATTTGTTATTCGCTCACAATTCACACAAATTCACACAAATTCACACAAATTC 2340
Db 2007 TGTGTGAAATTTGTTATTCGCTCACAATTCACACAAATTCACACAAATTCACACAAATTC 2066
Qy 2341 TAAAGCTTGGGTTGCCCTTAATGAGTGAAGTAACTCACAATTAATTCGCTTGGCTCACCTGCC 2400
Db 2067 TAAAGCTTGGGTTGCCCTTAATGAGTGAAGTAACTCACAATTAATTCGCTTGGCTCACCTGCC 2126
Qy 2401 CGCTTTCCAGTCCGGGAAACCTGTGCTGCGCAGCTGCAATTAATGAAATCGGCGCGG 2460
Db 2127 CGCTTTCCAGTCCGGGAAACCTGTGCTGCGCAGCTGCAATTAATGAAATCGGCGCGG 2186
Qy 2461 GAGAGCGGTTTTCGCTGTTTGGGCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTC 2520
Db 2187 GAGAGCGGTTTTCGCTGTTTGGGCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTC 2246
Qy 2521 GGTGCTTTCGCTTTCGCTGCGGCGGTATCAGCTCACTCAAAAGCGGTAAATCGGTTATCCAC 2580
Db 2247 GGTGCTTTCGCTTTCGCTGCGGCGGTATCAGCTCACTCAAAAGCGGTAAATCGGTTATCCAC 2306
Qy 2581 AGAATCAGGGAATAACGAGGAAAGAAATGTGAGCAAAAGCGCAGCAAAAGCGCAGAA 2640
Db 2307 AGAATCAGGGAATAACGAGGAAAGAAATGTGAGCAAAAGCGCAGCAAAAGCGCAGAA 2366
Qy 2641 CCGTAAAGGCGCGCTGCTGCGGTTTTTTCATAGGCTCCGCCCTCCGCTTTCGCTTTCGCTTTC 2700
Db 2367 CCGTAAAGGCGCGCTGCTGCGGTTTTTTCATAGGCTCCGCCCTCCGCTTTCGCTTTCGCTTTC 2426
Qy 2701 CAAAAATTCGACGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAAGATACCAAGC 2760
Db 2427 CAAAAATTCGACGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAAGATACCAAGC 2486
Qy 2761 GTTTCCCTCCGAGGCTCCCTGCTGCTCTCTGTTGCGACCTGCGCTTACCGGATA 2820
Db 2487 GTTTCCCTCCGAGGCTCCCTGCTGCTCTCTGTTGCGACCTGCGCTTACCGGATA 2546
Qy 2821 CCGTCCGCTTTCCTCCCTTCGGGAAGCGTGGCGTTTTCTCAATGCTCAAGCTGCTAGGATA 2880
Db 2547 CCGTCCGCTTTCCTCCCTTCGGGAAGCGTGGCGTTTTCTCAATGCTCAAGCTGCTAGGATA 2606
Qy 2881 TCTCAGTTCCGTTAGGTTGCTTCCGCTCAAGCTGGGCTGTGTGACGAAACCCCGCTTCA 2940
Db 2607 TCTCAGTTCCGTTAGGTTGCTTCCGCTCAAGCTGGGCTGTGTGACGAAACCCCGCTTCA 2666
Qy 2941 GCCCGACCGCTGGCGCTTATCCGTTAACTATCGCTTGTAGTCCAAACCCGCTAAGACGA 3000
Db 2667 GCCCGACCGCTGGCGCTTATCCGTTAACTATCGCTTGTAGTCCAAACCCGCTAAGACGA 2726
Qy 3001 CTTATCGCACCTGGCAGCAGCCACTGTAACAGGATTAGCAGAGGAGGTATGTAGGCGG 3060
Db 2727 CTTATCGCACCTGGCAGCAGCCACTGTAACAGGATTAGCAGAGGAGGTATGTAGGCGG 2786
Qy 3061 TGTACAGAGTTCTTGAAGTGGTGGCTAACTACGCTACACTAGAGGAGCAGTATTTGG 3120
Db 2787 TGTACAGAGTTCTTGAAGTGGTGGCTAACTACGCTACACTAGAGGAGCAGTATTTGG 2846
Qy 3121 TATCTGGCTCTGCTGAAAGCAGTTACCTTCGAAAAAAGTTGGTAGCTCTTGTATCCGG 3180
Db 2847 TATCTGGCTCTGCTGAAAGCAGTTACCTTCGAAAAAAGTTGGTAGCTCTTGTATCCGG 2906

Qy	2511	CGCTGCGCTCGGTCGTTCTGGCTCGGCGAGCGGTTATCAGTCTCACTCAAAAGCGCGTAATAC	2570
Db	3932	CGCTGCGCTCGGTCGTTCTGGCTCGGCGAGCGGTTATCAGTCTCACTCAAAAGCGCGTAATAC	3991
Qy	2571	GGTTATCCACAGAAATCAGGGGATAACCGCAGGAAAGAACATGTGACGAAAAAGGCCAGCAAA	2630
Db	3992	GGTTATCCACAGAAATCAGGGGATAACCGCAGGAAAGAACATGTGACGAAAAAGGCCAGCAAA	4051
Qy	2631	AGGCCAGGAACCGGTATAAAAGCCGCGTGTGCGTTTTCATAGGCTCCGCCCCCTG	2690
Db	4052	AGGCCAGGAACCGGTATAAAAGCCGCGTGTGCGTTTTCATAGGCTCCGCCCCCTG	4111
Qy	2691	ACGAGCATCACAAAATCGACGCTCAAGTCAGAGTGGGAAACCCGACAGGACTATAAA	2750
Db	4112	ACGAGCATCACAAAATCGACGCTCAAGTCAGAGTGGGAAACCCGACAGGACTATAAA	4171
Qy	2751	GATACACAGGGGTTTCCGCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCGACACCTGCCGC	2810
Db	4172	GATACACAGGGGTTTCCGCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCGACACCTGCCGC	4231
Qy	2811	TTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAAGCGTGGCGTTTCTCAATGCTCAC	2870
Db	4232	TTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAAGCGTGGCGTTTCTCAATGCTCAC	4291
Qy	2871	GCTGTAGGATCTCAGTTCGGTGTAGTCTGCTCCGTAACATCGTCTTGAGTCCAAACCCGG	2930
Db	4292	GCTGTAGGATCTCAGTTCGGTGTAGTCTGCTCCGTAACATCGTCTTGAGTCCAAACCCGG	4351
Qy	2931	CCCCGTTACGCCCCGACCGCTGGCGCTTATCCGGTAACATCGTCTTGAGTCCAAACCCGG	2990
Db	4352	CCCCGTTACGCCCCGACCGCTGGCGCTTATCCGGTAACATCGTCTTGAGTCCAAACCCGG	4411
Qy	2991	TAAACACAGACTTATCCGCACTGACACGCACTGTGTAAACAGATPACAGAGCGGAGGT	3050
Db	4412	TAAACACAGACTTATCCGCACTGACACGCACTGTGTAAACAGATPACAGAGCGGAGGT	4471
Qy	3051	ATGTAGCGCGTGTACAGAGTCTTGAGTGTGGCTTAACACTAGGCTACACTAGAGGA	3110
Db	4472	ATGTAGCGCGTGTACAGAGTCTTGAGTGTGGCTTAACACTAGGCTACACTAGAGGA	4531
Qy	3111	CAGTATTTGGTATCTGGGCTCTGCTGAAGCCAGTTACTCTCGGAAAAAGATTGGTAGCT	3170
Db	4532	CAGTATTTGGTATCTGGGCTCTGCTGAAGCCAGTTACTCTCGGAAAAAGATTGGTAGCT	4591
Qy	3171	CTTGATCCGGCAAAACAAACCAACCGCTGGTAGCGTGGTTTTTTTGTTCGAAGCAGCAGA	3230
Db	4592	CTTGATCCGGCAAAACAAACCAACCGCTGGTAGCGTGGTTTTTTTGTTCGAAGCAGCAGA	4651
Qy	3231	TTACGGCGCAAAAAAGAGTCTCAGAAATCCTTTGATCTTTTCTACGGGCTCTGACG	3290
Db	4652	TTACGGCGCAAAAAAGAGTCTCAGAAATCCTTTGATCTTTTCTACGGGCTCTGACG	4711
Qy	3291	CTCAGTGGAAACGAAAACTCAACGTTAAGGGATTTTGGTCATGAGCGGATACATATTTGAAT	3350
Db	4712	CTCAGTGGAAACGAAAACTCAACGTTAAGGGATTTTGGTCATGAGCGGATACATATTTGAAT	4771
Qy	3351	GTATTTAGAAAAATAACAAATATAGGGTTCCGGCGCATTTTCCCGGAAAGTGCCACCTG	3410
Db	4772	GTATTTAGAAAAATAACAAATATAGGGTTCCGGCGCATTTTCCCGGAAAGTGCCACCTG	4831
Qy	3411	TATGCGGTGTGAATACCGCACAGATCGGTAAAGGAAATAACCGCATCAGGAAATTGTA	3470
Db	4832	TATGCGGTGTGAATACCGCACAGATCGGTAAAGGAAATAACCGCATCAGGAAATTGTA	4891
Qy	3471	AGCGTTAATAATTCAGAAAGAACTCGTCAAGAAAGCGGATAGAAGCGGATCGCTGCGAATC	3530
Db	4892	AGCGTTAATAATTCAGAAAGAACTCGTCAAGAAAGCGGATAGAAGCGGATCGCTGCGAATC	4951
Qy	3531	GGAGCGCGGATACCGTAAAGCAAGAGGAAGCGGTACGCCATTCGCCGCCAAGCTCTTC	3590
Db	4952	GGAGCGCGGATACCGTAAAGCAAGAGGAAGCGGTACGCCATTCGCCGCCAAGCTCTTC	5011

QY	3591	AGCAATATACGGGTAGCCAAAGCTATGTCTCTGATAGCGGTCCGCCACACCCAGCCGGCC	3650
DB	5012	AGCAATATACGGGTAGCCAAAGCTATGTCTCTGATAGCGGTCCGCCACACCCAGCCGGCC	5071
QY	3651	ACAGTCGATGAATCCAGAAAGCGGCCATTTTCCACCATGATATTGGCAAGCAGGCGATC	3710
DB	5072	ACAGTCGATGAATCCAGAAAGCGGCCATTTTCCACCATGATATTGGCAAGCAGGCGATC	5131
QY	3711	GCCATGGGTCAACGACGAGATCCTCGCCGTGGGGCATGCTCGCCTTGAGCCTGCGCAACAG	3770
DB	5132	GCCATGGGTCAACGACGAGATCCTCGCCGTGGGGCATGCTCGCCTTGAGCCTGCGCAACAG	5191
QY	3771	TTCCGCTGGCGGAGGCCCTGATGCTCTTCGTTCAGATCATCTGTATCGACAAGACCGCG	3830
DB	5192	TTCCGCTGGCGGAGGCCCTGATGCTCTTCGTTCAGATCATCTGTATCGACAAGACCGCG	5251
QY	3831	TTCCATCCGAGTACGCTCGCTCGTCGATGCCATGTTTCGCTTGGTGGTTCGAATCGGCAGGT	3890
DB	5252	TTCCATCCGAGTACGCTCGCTCGTCGATGCCATGTTTCGCTTGGTGGTTCGAATCGGCAGGT	5311
QY	3891	AGCCGGATCAAGCGTATGACGCCCGCCATTTGCATCAGCCATGATGGATACTTTCTCGGC	3950
DB	5312	AGCCGGATCAAGCGTATGACGCCCGCCATTTGCATCAGCCATGATGGATACTTTCTCGGC	5371
QY	3951	AGGAGCAAGGTGAGATGACAGGAGATCTCTCCCGCGCATTTTCGCCCAATAGCAGCCAGTC	4010
DB	5372	AGGAGCAAGGTGAGATGACAGGAGATCTCTCCCGCGCATTTTCGCCCAATAGCAGCCAGTC	5431
QY	4011	CTTTCCCGCTTCAGTGACAACGTCGAGCAGCTGCGCAAGGAACGCCCGTCTGTGGCCAG	4070
DB	5432	CTTTCCCGCTTCAGTGACAACGTCGAGCAGCTGCGCAAGGAACGCCCGTCTGTGGCCAG	5491
QY	4071	CCACGATAGCGCGCTCGCTCGCTCTTGCAGTTCATTTCAGGGCACCCGACAGGTTCGTCTT	4130
DB	5492	CCACGATAGCGCGCTCGCTCGCTCTTGCAGTTCATTTCAGGGCACCCGACAGGTTCGTCTT	5551
QY	4131	GACAAAAGAACCGGGCGCCCTTCGCGTGAACGCCGGAACAACCGCGGCATCAGAGCAGCC	4190
DB	5552	GACAAAAGAACCGGGCGCCCTTCGCGTGAACGCCGGAACAACCGCGGCATCAGAGCAGCC	5611
QY	4191	GATTGTCGTGTGTGCCAGTTCATAGCCGATAGCCTTCACACCAAGCGCCGGAGACC	4250
DB	5612	GATTGTCGTGTGTGCCAGTTCATAGCCGATAGCCTTCACACCAAGCGCCGGAGACC	5671
QY	4251	TGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCTCTTCTTGATCAGA	4310
DB	5672	TGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCTCTTCTTGATCAGA	5731
QY	4311	GTTTGATCCCTCGCCATCAG	4332
DB	5732	GCTTGATCCCTCGCCATCAG	5753

```

RESULT 6
; US-10-811-028A:4
; Sequence 4, Application US/10811028A
; Publication No. US20050043258A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michael
; APPLICANT: Chen, Yen-Ju
; APPLICANT: Gentexic, Inc.
; TITLE OF INVENTION: Methods of Treating Xerostomia and Xerophthalmia
; FILE REFERENCE: 020714-002410US
; CURRENT APPLICATION NUMBER: US/10/811,028A
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US 60/458,793
; PRIOR FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 5760
; TYPE: DNA
; ORGANISM: Artificial Sequence

```



```

; FEATURE:
; ; OTHER INFORMATION: Description of Artificial Sequence:pMB1-Mt-CAT
; ; OTHER INFORMATION: plasmid expression vector
US-10-811-028A-4

```

Query Match 54.1%; Score 2341.8; DB 8; Length 5760;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2349; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

[illegible]

Qy	1581	CAAAGGGAGTTGCTGGAAGCCATCAAA	CGTGA	CTTTGGTTCTTTGACAAAGTTTAA	GA	1640
Db	1165	ACAAAGCCATCAGTGGTCTGC				1185
Qy	1641	GAAGCTACGGCTGCATCTGTTGGTGT	CAAGGCT	CAGGTTGGGGTTGGCTTGGTTTCA	A	1700
Db	1186					1223
Qy	1701	TAAGGAACGGGACACATTACAAAT	TGTCTT	GCTCCAAATCAGGATCCACTGCA	AGGAAC	1760
Db	1224	AAGGA	CTGATGCCCTCCAGAT			1247
Qy	1761	AACAGGCTTATTCCACTGCTGGGGA	TTGATGTGGGAGCAGCCTTACTAC	CTTCAGTA		1820
Db	1248					1269
Qy	1821	TAAAAATGTCAGGCTGATTATCT	TAAAGCTATT	TGGAATGTAATCAATGGGGAGAA	TG	1880
Db	1270	GCA	CACTCAGATGGATAC	TTTCTGCAAGCTCTTCGGGTCT	ACGCCA	1317
Qy	1881	TAACTGAAAGATACATGCGTTG	CAAAAAGTAAACCA	CGATGTTATGCTGGAAAAA	AAAAA	1940
Db	1318					1360
Qy	1941	AAAAAAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAA	AAACGGNATCCCTGCA	2000
Db	1361	CAGGAGGGGACAGGTGATC				1404
Qy	2001	GCCCGGGGATCCACTAGTTTCT	AGAGCGGCGCACCGCGGTGGAG	CTCCACAACTAGAA		2060
Db	1405	AAT	TGGGTGGCATCCCTGTGAC	CCCTCCCACTGCTCTCCTGGCC	TGGAAGTGGCCAC	1464
Qy	2061	TGCAGTGA	AAAAATGCTTATTTGTGAAAT	TTGTGATGCTATTTGCTTTATTTG	TATTAACCA	2120
Db	1465	TCCAGTGC	CCACCAAGCTGTCTCTAA	TAAAAATTAAGTTGCATCATTTGT	CTGACTAGGT	1524
Qy	2121	TTATAAGCTCAATATAACA	TAGTTAAACAATTGCA	TTTATGTTTTTCAGGTTCA	G	2180
Db	1525	GTCTTCTATATATATTTG	GGGTGGAGGGGTGGTATGGAGCA	AGGGGCAAGTTGGGA		1584
Qy	2181	GGGAGGTGTGGGAGGTTTTT	TAAAGCCACAGCTCCAGCT	TTTTGTTCCCTTTAGTGAGGT		2240
Db	1585	GACAACTGTAGGCTCG	AGGGGGGGCCGGTAC	CAGCTTTGTTCCCTTTAGTGAGGT		1644
Qy	2241	TAA	TTTCGAGCTTCGGCTTAATCAT	GTGTATAGCTGTTCTCTGTGTAAT	TGTTATCCCG	2300
Db	1645	TAA	TTTCGAGCTTCGGGTAAATCAT	GTGTATAGCTGTTCTCTGTGTAAT	TGTTATCCCG	1704
Qy	2301	TCACAA	TTCCACACATACGAGCCGGA	AGCATAAAGTGTAAAGCTCGGGGTGCCTAAT		2360
Db	1705	TCACAA	TTCCACACATACGAGCCGGA	AGCATAAAGTGTAAAGCTCGGGGTGCCTAAT		1764
Qy	2361	GAGTGAGCTAATCAATTA	ATTGCGTTGCGCTCACTG	CCCGCTTCCAGTCGGGA	AACC	2420
Db	1765	GAGTGAGCTAATCAATTA	ATTGCGTTGCGCTCACTG	CCCGCTTCCAGTCGGGA	AACC	1824
Qy	2421	TGT	CGTGCCAGCTGATTAATGAAT	TCGSCAAACCGCGGAGAGCGGTTTGGGTATTG		2480
Db	1825	TGT	CGTGCCAGCTGATTAATGAAT	TCGSCAAACCGCGGAGAGCGGTTTGGGTATTG		1884
Qy	2481	GGCGCT	TTTCGCTTCTCGCTCACTG	ATCGCTCGCTCGGTCGGTCTCGGCTGCGCGAG		2540
Db	1885	GGCGCT	TTTCGCTTCTCGCTCACTG	ATCGCTCGCTCGGTCGGTCTCGGCTGCGCGAG		1944
Qy	2541	CGGTAT	CAGCTCACTCAAGCGGTTATAC	GGTTATCCACAGATCAGGGGATAAC	CGAG	2600
Db	1945	CGGTAT	CAGCTCACTCAAGCGGTTATAC	GGTTATCCACAGATCAGGGGATAAC	CGAG	2004
Qy	2601	GAAAGAA	CATGTGAGCAAAAGCCAGCA	AAAAAGGCGCAGGAAACCGTAAAAA	AGCCCGCTGTC	2660
Db	2005	GAAAGAA	CATGTGAGCAAAAGCCAGCA	AAAAAGGCGCAGGAAACCGTAAAAA	AGCCCGCTGTC	2064

Qy	2661	TGCGGTTTTTCATAGGCTCGCGCCCTCGACGAGCATCACAAAATTCAGCGTCAAGTC	2722
Db	2065	TGCGGTTTTTCCATAGGCTCGCGCCCTCGACGAGCATCACAAAATTCAGCGTCAAGTC	2124
Qy	2721	AGAGGTGGCGAAACCCGACAGGACTATAAGATACACAGCGTTTCCCTCGGAAGCTCC	2780
Db	2125	AGAGGTGGCGAAACCCGACAGGACTATAAGATACACAGCGTTTCCCTCGGAAGCTCC	2184
Qy	2781	TCGTGGCTCTCTGTTTCGAACCTCGCGGTTTACCGGATACCTGTCCGCTTCTCCCTT	2840
Db	2185	TCGTGGCTCTCTGTTTCGAACCTCGCGGTTTACCGGATACCTGTCCGCTTCTCCCTT	2244
Qy	2841	CGGGAAGCGTGGCGCTTTCTCAATGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTG	2900
Db	2245	CGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTG	2304
Qy	2901	TTCCGCTCAAAGCTGGCTGTGTGCAGCAACCCCGCTTTCAGCCCGACCGCTGCGCTTAT	2960
Db	2305	TTCCGCTCAAAGCTGGCTGTGTGCAGCAACCCCGCTTTCAGCCCGACCGCTGCGCTTAT	2364
Qy	2961	CCGGTAACATCGTCTTGAGTCCAAACCCGTAAGACACGACTTATCGCCACTGGCAGCAG	3020
Db	2365	CCGGTAACATCGTCTTGAGTCCAAACCCGTAAGACACGACTTATCGCCACTGGCAGCAG	2424
Qy	3021	CCACTGTTAAACAGATTTAGCAGCAGCAGGTATGTAGCCGCTGTACAGAGTCTTTGAAAT	3080
Db	2425	CCACTGTTAAACAGATTTAGCAGCAGCAGGTATGTAGCCGCTGTACAGAGTCTTTGAAAT	2484
Qy	3081	GGTGGCCTAACTACGGCTACACTAGAAGGACGATTTTGGTATCTCGCTCTGCTCAAGC	3140
Db	2485	GGTGGCCTAACTACGGCTACACTAGAAGGACGATTTTGGTATCTCGCTCTGCTCAAGC	2544
Qy	3141	CAGTTACTCTTGGAAAAGAGTTGGTAGCTCTTTGATCCGGCAAAACAAACACCGCTGGTA	3200
Db	2545	CAGTTACTCTTGGAAAAGAGTTGGTAGCTCTTTGATCCGGCAAAACAAACACCGCTGGTA	2604
Qy	3201	CGCGTGGTTTTTTTGTGTAACGACGAGATTTACGGCAGAAAAAAGGATCTCAAGAG	3260
Db	2605	CGCGTGGTTTTTTTGTGTAACGACGAGATTTACGGCAGAAAAAAGGATCTCAAGAG	2664
Qy	3261	ATCCCTTTGATCTTTCTACGGGCTCTACGCTCAGTGGAAACGAAATCTCAAGAA	3320
Db	2665	ATCCCTTTGATCTTTCTACGGGCTCTACGCTCAGTGGAAACGAAATCTCAAGAA	2695
Qy	3321	TTTTGGTCATGAGCGGATACATATTTGAAATGTATTTAGAAAAATAACAATAGGGGTC	3380
Db	2696	TTTTGGTCATGAGCGGATACATATTTGAAATGTATTTAGAAAAATAACAATAGGGGTC	2695
Qy	3381	CGCGCACATTTCCCGAAAAGTGCCACCTGTATCGCGGTGTGAATACCGCACAGATCGGT	3440
Db	2696	CGCGCACATTTCCCGAAAAGTGCCACCTGTATCGCGGTGTGAATACCGCACAGATCGGT	2695
Qy	3441	AAGGAGAAATACCGCATCAGGAAATTTGAAGCGTTAAATAATTCAGAAGAACTCGTCAAG	3500
Db	2696	AAGGAGAAATACCGCATCAGGAAATTTGAAGCGTTAAATAATTCAGAAGAACTCGTCAAG	2713
Qy	3501	AAGGCGATAGAAAGCGATGCGCTCGGAATCGGGAGCGCGCATACCGTTAAAGCAGAGAA	3560
Db	2714	AAGGCGATAGAAAGCGATGCGCTCGGAATCGGGAGCGCGCATACCGTTAAAGCAGAGAA	2773
Qy	3561	CGGCTCAGCCCATTTGCGCGCCCAAGCTCTTCAGCAATATCACGGGTAGCCAAACGCTATGTC	3620
Db	2774	CGGCTCAGCCCATTTGCGCGCCCAAGCTCTTCAGCAATATCACGGGTAGCCAAACGCTATGTC	2833
Qy	3621	CTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTTCGATGAATCCAGAAAGCGGCCATT	3680
Db	2834	CTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTTCGATGAATCCAGAAAGCGGCCATT	2893
Qy	3681	TTCCACCATGATATTTCCGACAGCAGGCATCGCCATGCTCAGCAGAGATCTCTCGCGCTC	3740
Db	2894	TTCCACCATGATATTTCCGACAGCAGGCATCGCCATGCTCAGCAGAGATCTCTCGCGCTC	2953
Qy	3741	GGGCATGCTCGCCCTTGAGCCTTGGCGAAACAGTTTCGGCTGGCGCGAGCCCCATGCTCTTC	3800

QY	1340	ACGACTACGGCGCCTTGAACTCACAATCAACGGCGCAGATCATCAGCTGCACACAGCA	1399	QY	2420	CTGTCTGCAGCTGCATTAATGAATCGGCAACGGCGGGGAGAGCGGTTTCGGTATT	2479
Db	822	AGCTGCTCTGTGGCTGTGATCTGCCTCAAAACCCAGACGCTGGGTAGCAGGAGACCTTG	881	Db	1779	CTGTCTGCAGCTGCATTAATGAATCGGCAACGGCGGGGAGAGCGGTTTCGGTATT	1838
QY	1400	AGCAACCGCGGCTACGTGAAACCACTGAACGTCAACGAGGAGAAGTACAGAGGGGT	1459	QY	2480	GGGCGCTCTTCGGCTTCTCGCTCACTGACTCGCTGCGCTCGGTCTGCTTCGGCTCGGCGA	2539
Db	882	ATGCTCTCTGGCACAGATGAGGAGAATCTCTCTTTCTCTCTCTTTGAAGAACAGA	935	Db	1839	GGGCGCTCTTCGGCTTCTCGCTCACTGACTCGCTGCGCTCGGTCTGCTTCGGCTCGGCGA	1898
QY	1460	TGGCCAAAGGAGATGTTACACCCAGATAGCTCTTCAGCCTGCATGAAGTTCAATGGTG	1519	QY	2540	GCGTATCAGCTACTCAAAAGGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACGCA	2599
Db	936	-----CATGAATTTGGATTTCCCAAGGAGGAGTTTGGCAACAGTTCCAAAGGCTGAA	990	Db	1899	GCGTATCAGCTACTCAAAAGGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACGCA	1958
QY	1520	GTGGTCATATCAATCATAGCAATTTCTGGCAAAACCTCAGCCCTAACGGTGGTGAGAAC	1579	QY	2600	GGAAAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCGCAGGACCCCTAAAGGCGCGTTG	2659
Db	991	CCATCCCTGTCTCCATGAGATGATCCAGCAGATCTTCAATCTCTTCAGCACAAAGGACT	1050	Db	1959	GGAAAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCGCAGGACCCCTAAAGGCGCGTTG	2018
QY	1580	CAAAGGGGAGTTGCTGGAAGGCATCAAAAGTGACTTTGGTTCTTTGACAAAGTTAAGG	1639	QY	2660	CTGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGT	2719
Db	1051	CATCTGCTGCTTGGGATGAGACCCCTCTAGACAAATTTCTACACTGAATCTTACCAGCAGC	1110	Db	2019	CTGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGT	2078
QY	1640	AGAAGTCAGCGCTGCACTGTGTGTGTGTCAGAGCTCAGGTTGGGTTGGCTTGGTTTCA	1699	QY	2720	CAGAGTGGGGAACCCGACAGGACTATAAAGATAACAAGGCTTTCCCTTGGAAAGTCC	2779
Db	1111	TGAATGAACCTGAAGCCTGTGT-----GATACAGGGGTTGGGTTGACAGACTCCC	1163	Db	2079	CAGAGTGGGGAACCCGACAGGACTATAAAGATAACAAGGCTTTCCCTTGGAAAGTCC	2138
QY	1700	ATAAGGAACGGGACACTTACAAATTTGCTGTGTCTGTCTTGTCCAAATCAGGATCCACTGCAAGAA	1759	QY	2780	CTGCTGCGCTCTCTGTTCCGACCTGCGCTTACCGGATACCTGTCCGCTTTCTCCCT	2839
Db	1164	CTGATGAAGGAGGACTC-----	1180	Db	2139	CTGCTGCGCTCTCTGTTCCGACCTGCGCTTACCGGATACCTGTCCGCTTTCTCCCT	2198
QY	1760	CAACAGGCTTATTTCCACTGTCTGGGGATGATGTGGGAGCACGCTTACTCTTCACT	1819	QY	2840	TCGGAGAGCTGGCGCTTTCTCAATGTCTCAGCTGTAGGTATCTCAGTTCCGTTGAGTGC	2899
Db	1181	-----CATTTCTGGCTGTGAGGAAATATCTTCCAAAGAAATCACTCTCTATCTGAAAG	1230	Db	2199	TCGGAGAGCTGGCGCTTTCTCAATGTCTCAGCTGTAGGTATCTCAGTTCCGTTGAGTGC	2258
QY	1820	ATAAATATCTCAGGCTGATTTATCTAAAGCTATTGGAAATGTAATCAATCACTGGGAGAT	1879	QY	2900	GTTCTGCTCAAGCTGGGCTGTGTGCAAAACCCCGTTTCCGCTTCCGCTTCCGCTTCA	2959
Db	1231	AGAGAAATACAGCCCTTGTGCTGGGAGTTGTGAGAGCAAAATCATGATCTTTT	1290	Db	2259	GTTCTGCTCAAGCTGGGCTGTGTGCAAAACCCCGTTTCCGCTTCCGCTTCCGCTTCA	2318
QY	1880	GTAACTGAAGATACATGGCTTGCAGAAAGTAAACCAAGATCGTTATGCTGGAAAAAAA	1939	QY	2960	TCGGTAACTATCTGTTGAGTCCAAACCGGTAGACACAGCTTATCCCACTGGCAGCA	3019
Db	1291	CTTTGTC-----A	1298	Db	2319	TCGGTAACTATCTGTTGAGTCCAAACCGGTAGACACAGCTTATCCCACTGGCAGCA	2378
QY	1940	AAA	1999	QY	3020	GCCACTGTATAACAGGATTAGCAGACGAGGTATGTAGCGGTGTCTACAGATTCTTGAAG	3079
Db	1299	ACAAATCTTGAAGAAAGTTTAAAGAGTAAGGAATGAATCTAGAAAGCGGAATTTGCGAG	1358	Db	2379	GCCACTGTATAACAGGATTAGCAGACGAGGTATGTAGCGGTGTCTACAGATTCTTGAAG	2438
QY	2000	AGCCCGGGGATCCACTAGTTCTAGAGCGCGCCCAACCGGTGGAGCTCCCAAACTAGA	2059	QY	3080	TGGTGGCTAACTACGCTACACTAGAAAGACAGTATTTGGTATCTGCGCTCTGCTGAAG	3139
Db	1359	GAATTTGGGTGGCATCCCTGTGACCCCTCCCAAGTGCCTCTCTGGCCCTGGAAGTGCCA	1418	Db	2439	TGGTGGCTAACTACGCTACACTAGAAAGACAGTATTTGGTATCTGCGCTCTGCTGAAG	2498
QY	2060	ATGCAAGTAAATAATGCTTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAAAC	2119	QY	3140	CCAGTTTACCTTCGGGAAAGAGTTGGTAGCTCTTGCATCCGCAAAACCAACCACTGGT	3199
Db	1419	CTCCAGTGCACACGCTTGTCTTAAATAAATTAAGTTGATCATTTTGTCTGACTAGG	1478	Db	2499	CCAGTTTACCTTCGGGAAAGAGTTGGTAGCTCTTGCATCCGCAAAACCAACCACTGGT	2558
QY	2120	ATTTAAGTGCATTAACAGTTTAAACAATTTGATTCATTTTATGTTTTCAGTTTCAAG	2179	QY	3200	AGCGTGGTTTTTTTTTGTGAAAGCAGCAGATTTACGCGAGAAAAAAGGATCTCAAGAA	3259
Db	1479	TGCTCTCTTATAATATTTATGGGTGGAGGGGGTGGTATGAGCAAGGGGCAAGTTGGGA	1538	Db	2559	AGCGTGGTTTTTTTTTGTGAAAGCAGCAGATTTACGCGAGAAAAAAGGATCTCAAGAA	2618
QY	2180	GGGAGGTGTGGAGGTTTTTAAAGCCACAGCTCCAGCTTTTGTCCCTTTAGTGAGGG	2239	QY	3260	GATCTTTGATCTTTTCTACGGGCTGACCGCTCAGCGCTAGTGAACGAAAACTCAGCTTAAGGG	3319
Db	1539	AGACAACTGTAGGGCTCCAGGGGGGGCCCGGTACACAGTTTGTCCCTTTAGTGAGGG	1598	Db	2619	GATCTTTGATCTTTTCTACGGGCTGACCGCTCAGCGCTAGTGAACGAAAACTCAGCTTAAGGG	2650
QY	2240	TTAATTTGAGCTTGGCGTAATCATGCTCATAGCTGTTTCTGTGTGAAATTTATCCG	2299	QY	3320	ATTTTGGTTCATGAGCGGATACATATTTGAAATGATAATTTAGAAAAATAAATAAGGGGTT	3379
Db	1599	TTAATTTGAGCTTGGCGTAATCATGCTCATAGCTGTTTCTGTGTGAAATTTATCCG	1658	Db	2651	-----	2650
QY	2300	CTCACAAATTTCCACAAATACGAGCGGAGCATAAAGTGTAAAGCCTGGGGTGCCTAA	2359	QY	3380	CCGCGCACTTTTCCCGAAAAAGTGCCACTGTATCGGTGTGAAATAACGCAAGATCGG	3439
Db	1659	CTCACAAATTTCCACAAATACGAGCGGAGCATAAAGTGTAAAGCCTGGGGTGCCTAA	1718	Db	2651	-----	2650
QY	2360	TGAGTGAGCTAACTCACTAATTTGCGCTTCTGCGCTCACTGCGCTTTTCCAGTGGGAAAC	2419	QY	3440	TAAGGAGAAAAATACCGCATCAGGAAATTTGTAAGCGTTAATAATTCAGAAAGACTCGTCAA	3499
Db	1719	TGAGTGAGCTAACTCACTAATTTGCGCTTCTGCGCTCACTGCGCTTTTCCAGTGGGAAAC	1778	Db	2651	-----TCAGAAAGACTCGTCAA	2667
QY				QY	3500	GAAGGCGATAGAAGGCGATGCGCTGCGAATCGGAGCGGCGATACCGTAAAGCACGAGGA	3559


```

Db 2651 ----- 2650
Qy 3441 AAGGAGAAATACCGCATCAGAAATGTTAAGCGTTAATAATTCAGAGAACTCGTCAAG 3500
Db 2651 -----TCAGAGAACTCGTCAAG 2668
Qy 3501 AAGCGATAGAGCGGATGCGCTCGAATCGGAGCGCGGATACCGTAAAGACGAGGAA 3560
Db 2669 AAGCGATAGAGCGGATGCGCTCGAATCGGAGCGCGGATACCGTAAAGACGAGGAA 2728
Qy 3561 GCGGTACGCCATTCGCGCGCAAGCTTTCAGCAATATCAGGATGATCAGGATGATGTC 3620
Db 2729 GCGGTACGCCATTCGCGCGCAAGCTTTCAGCAATATCAGGATGATCAGGATGATGTC 2788
Qy 3621 CTGATAGCGGTCCGCCACACCGCGCGCAAGCTTTCAGCAATATCAGGATGATGTC 3680
Db 2789 CTGATAGCGGTCCGCCACACCGCGCGCAAGCTTTCAGCAATATCAGGATGATGTC 2848
Qy 3681 TTCACCATGATATTCGCAAGCAGGATCGCCATGCTCAGCAGAGATCCTCGCGGTC 3740
Db 2849 TTCACCATGATATTCGCAAGCAGGATCGCCATGCTCAGCAGAGATCCTCGCGGTC 2908
Qy 3741 GGGCATGCTCGCTTGAGCGCTGCGCAACAGTTCGGCTGGCGGAGCCCTGATGCTTTC 3800
Db 2909 GGGCATGCTCGCTTGAGCGCTGCGCAACAGTTCGGCTGGCGGAGCCCTGATGCTTTC 2968
Qy 3801 GTCCAGATCATCTGATCGCAACAGCGGCTTCCATCCGAGTACGTCTCGCTCGATGCG 3860
Db 2969 GTCCAGATCATCTGATCGCAACAGCGGCTTCCATCCGAGTACGTCTCGCTCGATGCG 3028
Qy 3861 ATGTTTCGTTGGTGGTTCGATGCGGATGCGGATCAAGCGTATGCGAGCGCGCAT 3920
Db 3029 ATGTTTCGTTGGTGGTTCGATGCGGATGCGGATCAAGCGTATGCGAGCGCGCAT 3088
Qy 3921 TGCAATCAGCATGATGATCTTCTCGGAGGAGCAAGTTCGATGATGATGATGATGATC 3980
Db 3089 TGCAATCAGCATGATGATCTTCTCGGAGGAGCAAGTTCGATGATGATGATGATGATC 3148
Qy 3981 CCCCGGACATTCGCCCAATAGCAGCAGTCCCTTCCCGCTTTCAGTGACAACTGAGCAC 4040
Db 3149 CCCCGGACATTCGCCCAATAGCAGCAGTCCCTTCCCGCTTTCAGTGACAACTGAGCAC 3208
Qy 4041 AGCTGCGCAAGGAAACCGCTGCTGCGGAGCAGATAGCGGCTGCTGCTGCTGCTGCTG 4100
Db 3209 AGCTGCGCAAGGAAACCGCTGCTGCGGAGCAGATAGCGGCTGCTGCTGCTGCTGCTG 3268
Qy 4101 TTCAATTCAGGCAACCGGACAGGTCGCTTTCGACAAAGAACCGGCGGCGCTGCGCTGA 4160
Db 3269 TTCAATTCAGGCAACCGGACAGGTCGCTTTCGACAAAGAACCGGCGGCGCTGCGCTGA 3328
Qy 4161 CAGCGGAAACACCGGCGCATCAGAGCAGCGATGCTGTTGTCGCCAGTATAGCGGAA 4220
Db 3329 CAGCGGAAACACCGGCGCATCAGAGCAGCGATGCTGTTGTCGCCAGTATAGCGGAA 3388
Qy 4221 TAGCTTTCACCAAGCGCGGAGAACTGCTGCAATCCATCTTGTTCATATGATGCG 4280
Db 3389 TAGCTTTCACCAAGCGCGGAGAACTGCTGCAATCCATCTTGTTCATATGATGCG 3448
Qy 4281 AAACGATCTCATCTGCTCTTTCATCAGAGCTTGTATCCCTGCGCATCAG 4332
Db 3449 AAACGATCTCATCTGCTCTTTCATCAGAGCTTGTATCCCTGCGCATCAG 3500

```

RESULT 10
 US-10-198-478-16
 ; Sequence 16, Application US/10198478
 ; Publication No. US2003018836A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corbin, David R.
 ; APPLICANT: Romano, Charles P.
 ; TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotoxin
 ; FILE REFERENCE: 38-21 (13547) B
 ; .CURRENT APPLICATION NUMBER: US/10/198,478

```

; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/186, 002
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 16
; LENGTH: 8349
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: completely synthesized
; NAME/KEY: misc feature
; LOCATION: (1)..(8349)
; OTHER INFORMATION:
US-10-198-478-16

```

Query Match 42.6%; Score 1845.4; DB 6; Length 8349;
 Best Local Similarity 92.6%; Pred. No. 0;
 Matches 1983; Conservative 0; Mismatches 101; Indels 57; Gaps 2;

```

Qy 2249 AGCTTCGCGTAAATCATGCTCATAGCTGTTTCCTGTGTGAATTTGTTATCCGCTCACAAATT 2308
Db 5909 AGCTTCGCGTAAATCATGCTCATAGCTGTTTCCTGTGTGAATTTGTTATCCGCTCACAAATT 5968
Qy 2309 CCACACAAATACGAGCGGAGCAATAAAGTGTAAAGCCTGGGTGCTTAATGAGTGAGC 2368
Db 5969 CCACACAAATACGAGCGGAGCAATAAAGTGTAAAGCCTGGGTGCTTAATGAGTGAGC 6028
Qy 2369 TAACTCACATTAATTCGTTGCGCTCACTGCCCGCTTTCAGTCCGGAACCTGTCTGTC 2428
Db 6029 TAACTCACATTAATTCGTTGCGCTCACTGCCCGCTTTCAGTCCGGAACCTGTCTGTC 6088
Qy 2429 CAGCTCATTAATGAATCGGCAACCGCGGGGAGGCGGTTTTCGTTATTTGGCGCTCT 2488
Db 6089 CAGCTCATTAATGAATCGGCAACCGCGGGGAGGCGGTTTTCGTTATTTGGCGCTCT 6148
Qy 2489 TCCTGCTTCCTGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCA 2548
Db 6149 TCCTGCTTCCTGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCA 6208
Qy 2549 GCTCACTCAAGCGGTAATAACGTTATCCAGAAATACAGGGATTAACAGAGAAAGAAC 2608
Db 6209 GCTCACTCAAGCGGTAATAACGTTATCCAGAAATACAGGGATTAACAGAGAAAGAAC 6268
Qy 2609 ATGTGAGCAAAAGCGGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2668
Db 6269 ATGTGAGCAAAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6328
Qy 2669 TTCCATAGGCTCCGCGCGCTGACGAGCATCAAAATACAGCGCTCAAGTCAAGAGGTGG 2728
Db 6329 TTCCATAGGCTCCGCGCGCTGACGAGCATCAAAATACAGCGCTCAAGTCAAGAGGTGG 6388
Qy 2729 CGAAACCCGACAGGATATAAAGATACAGGCGTTTCCCTCGGAGAGCTCCCTCGTGGC 2788
Db 6389 CGAAACCCGACAGGATATAAAGATACAGGCGTTTCCCTCGGAGAGCTCCCTCGTGGC 6448
Qy 2789 TCTCTGTTCCGACCGCTGCGGATACCGGATACCTGTCGCGCTTTCCTCCCTCGGAGAGC 2848
Db 6449 TCTCTGTTCCGACCGCTGCGGATACCGGATACCTGTCGCGCTTTCCTCCCTCGGAGAGC 6508
Qy 2849 GTGGCGCTTTCCTCAATGCTCACTGCTAGGATATCTCAGTTTCGTTGAGTGTGCTTCGCTCC 2908
Db 6509 GTGGCGCTTTCCTCAATGCTCACTGCTAGGATATCTCAGTTTCGTTGAGTGTGCTTCGCTCC 6568
Qy 2909 AAGCTGGCTGTGTGACGAAACCCCGCTTTCAGCGAGCGCTGCGCTTATTCGGTAAAC 2968
Db 6569 AAGCTGGCTGTGTGACGAAACCCCGCTTTCAGCGAGCGCTGCGCTTATTCGGTAAAC 6628
Qy 2969 TATCGTCTTGTGAGTCCAAACCGGTAAGACAGACTTATCGCACTGGCAGCAGGACCTGGT 3028
Db 6629 TATCGTCTTGTGAGTCCAAACCGGTAAGACAGACTTATCGCACTGGCAGCAGGACCTGGT 6688

```

QY 3029 AACAGGATTAGCAGAGCGAGGTATGTAGCGGCTGCTACAGAGTTCTTTGAAGTGTGGCCT 3088
DB |||||
QY 6689 AACAGGATTAGCAGAGCGAGGTATGTAGCGGCTGCTACAGAGTTCTTTGAAGTGTGGCCT 6748
DB |||||
QY 3089 AACTACGGCTACACTAGAGGACAGTATTTGGTATCTGGCGTCTGCTGAGAGCCAGTTACC 3148
DB |||||
QY 6749 AACTACGGCTACACTAGAGGACAGTATTTGGTATCTGGCGTCTGCTGAGAGCCAGTTACC 6808
DB |||||
QY 3149 TTCGGAAGAGTTGGTGTAGCTCTTTGATCCGGCAAAACAAACACCGCTGGTGTAGCGGTGGT 3208
DB |||||
QY 6809 TTCGGAAGAGTTGGTGTAGCTCTTTGATCCGGCAAAACAAACACCGCTGGTGTAGCGGTGGT 6868
DB |||||
QY 3209 TTTTGTGTTTCAAGCAGCAGATTAACGCGCAGAGAAAAAAGGATCTCAAGAAAGATCCCTTTG 3268
DB |||||
QY 6869 TTTTGTGTTTCAAGCAGCAGATTAACGCGCAGAGAAAAAAGGATCTCAAGAAAGATCCCTTTG 6928
DB |||||
QY 3269 ATCTTTTCTACGGGGTCTGACGCTCAGTGGAGCAAGAACTCAGTTAAGGATTTTGGTC 3328
DB |||||
QY 6929 ATCTTTTCTACGGGGTCTGACGCTCAGTGGAGCAAGAACTCAGTTAAGGATTTTGGTC 6988
DB |||||
QY 3329 ATGAGCGGATACATATTTGAATGTATTTAGA----- 3359
DB |||||
QY 6989 ATGAGATTATCAAAAGGATCTTACCTAGATCCTTTTGGGGTGGCGAAGAACTCCAGC 7048
DB |||||
QY 3360 -----AAATAAACAAATAGGGTTTCGGGCACATTTCCCGAANAAG 3401
DB |||||
QY 7049 ATGAGATCCCGCGCTGGAGGATCATCCAGCGCGCTCCCGAANAACGATTCGGAAGCCC 7108
DB |||||
QY 3402 TGCCACCTGTATCGGTG-----TGAATACCGCACAGATGCGTAAAGGAGAAAT 3451
DB |||||
QY 7109 AACCTTTTCATGAAGGGCGGCGTGAATCGAAATCTCGTATGGCAGTTGGGGTCTGCT 7168
DB |||||
QY 3452 ACCGCATCAGGAAATTTGAAGCGTTAATAATCAGAAGAACTCGTCAAGAGAGCGGATAGA 3511
DB |||||
QY 7169 TGGTCGTCATTTCGAACCCAGAGTCCGCTCAGAGAACTCGTCAAGAGGCGATAGA 7228
DB |||||
QY 3512 AGGCGATCGCTCGAAATCGGAGCGGCGATAACGTTAAAGCAAGAGGAGCGGTGAGCCC 3571
DB |||||
QY 7229 AGGCGATCGCTCGAAATCGGAGCGGCGATACCGTTAAAGCAAGAGGAGCGGTGAGCCC 7288
DB |||||
QY 3572 ATTCGCGCCAGCTCTTCAGCAATATCACGGTAGCCCAAGCTATGCTCTGTATGACGGT 3631
DB |||||
QY 7289 ATTCGCGCCAGCTCTTCAGCAATATCACGGTAGCCCAAGCTATGCTCTGTATGACGGT 7348
DB |||||
QY 3632 CGGCGACACCCAGCGGCGCACAGTGCATGAATCCAGAAAAAGCGGCATTTTCCACCATGA 3691
DB |||||
QY 7349 CGGCGACACCCAGCGGCGCACAGTGCATGAATCCAGAAAAAGCGGCATTTTCCACCATGA 7408
DB |||||
QY 3692 TATTCGGCAAGCAGGCATGCGCATGGGTACAGACAGATCTTCGCGCTCGGCGATGCTCG 3751
DB |||||
QY 7409 TATTCGGCAAGCAGGCATGCGCATGGGTACAGACAGATCTTCGCGCTCGGCGATGCTCG 7468
DB |||||
QY 3752 CCTTCAGCTGCGCAACAGTTTCGGCTGGCGGAGCCCTGTATGCTCTTCGTCCAGATCAT 3811
DB |||||
QY 7469 CCTTCAGCTGCGCAACAGTTTCGGCTGGCGGAGCCCTGTATGCTCTTCGTCCAGATCAT 7528
DB |||||
QY 3812 CCTGATCGAAGACCGGCTTCCATCCGAGTACGTCTCGCTCGATGCGATGTTTCGCTT 3871
DB |||||
QY 7529 CCTGATCGAAGACCGGCTTCCATCCGAGTACGTCTCGCTCGATGCGATGTTTCGCTT 7588
DB |||||
QY 3872 GGTGTGCAATGGGCAAGGTAGCCGATCAAGGTATGCGAGCCGCGCATTTGATCAGCCA 3931
DB |||||
QY 7589 GGTGTGCAATGGGCAAGGTAGCCGATCAAGGTATGCGAGCCGCGCATTTGATCAGCCA 7648
DB |||||
QY 3932 TGATGGATATTTTCTCGGAGGAGCAAGGTGAGATGACAGGAGATCTTCCCGCGCACCTT 3991
DB |||||
QY 7649 TGATGGATATTTTCTCGGAGGAGCAAGGTGAGATGACAGGAGATCTTCCCGCGCACCTT 7708
DB |||||
QY 3992 CGCCCAATAGCAGCCAGTCCCTTCCGCTTTCAGTGAACAAGTGCAGCAACAGTTCGCGAAG 4051
DB |||||
QY 7709 CGCCCAATAGCAGCCAGTCCCTTCCGCTTTCAGTGAACAAGTGCAGCAACAGTTCGCGAAG 7768
DB |||||
QY 4052 GAAACGCCCTCGTGGCCAGCCACGATAGCGCGCTGCTCTTCGAGTTCAATTCAGGG 4111
DB |||||

DB 7769 GAACGCCGCTCGTGGCCAGCACGATAGCCGCTGCTCGTCTGCAGTTCAATTCAGGG 7828
QY 4112 CACCGGACAGTCTGGTCTTGACAAAAAGAACCGGGCGCCCTGCGCTGACAGCCGGAACA 4171
DB 7829 CACCGGACAGTCTGGTCTTGACAAAAAGAACCGGGCGCCCTGCGCTGACAGCCGGAACA 7888
QY 4172 CGCGGCGATCAGAGCAGCCGATTTGTGTGTGCCAGTCATAGCCGAATAGCTCTTCCA 4231
DB 7889 CGCGGCGATCAGAGCAGCCGATTTGTGTGTGCCAGTCATAGCCGAATAGCTCTTCCA 7948
QY 4232 CCBAAGCGCGGAGAACCTTCCGTCGATCCATCTTCTCAATCATCGAAACGATCCTC 4291
DB 7949 CCCAAGCGCGGAGAACCTTCCGTCGATCCATCTTGTTCATCATCGAAACGATCCTC 8008
QY 4292 ATCTGTCTCTTGATCAGAGCTTGCATCCCTGCGCCATCAG 4332
DB 8009 ATCTGTCTCTTGATCAGATCTTGATCCCTGCGCCATCAG 8049
DB |||||
RESULT 11
US-10-841-796-33
; Sequence 33, Application US/10841796
; Publication No. US20040237138A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Biotechnology Corporation
; APPLICANT: Monsanto Technology LLC
; APPLICANT: Nordine, Chiekh
; APPLICANT: Fisher, Dane
; APPLICANT: Thompson, Rebecca
; TITLE OF INVENTION: A method of increasing yield in a plant
; FILE REFERENCE: Docket number 38-21(15691)B
; CURRENT APPLICATION NUMBER: US/10/841.796
; CURRENT FILING DATE: 2004-07-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 11546
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid containing construct for corn transformation
US-10-841-796-33
Query Match 42.6%; Score 1845.4; DB 8; Length 11546;
Best Local Similarity 92.6%; Pred. No. 0;
Matches 1983; Conservative 0; Mismatches 101; Indels 57; Gaps 2;
QY 2249 AGCTTGGCGTAAATCATGCTCATAGCTGTTCTCTGTGTAATTTGTTATCCGCTCACAATT 2308
DB |||||
QY 9106 AGCTTGGCGTAAATCATGCTCATAGCTGTTCTCTGTGTAATTTGTTATCCGCTCACAATT 9165
DB |||||
QY 2309 CCACAACAATACAGAGCCGGAAGCATAAAGTGTAAAGCTTGGGTGCTTAATGAGTGAGC 2368
DB 9166 CCACAACAATACAGAGCCGGAAGCATAAAGTGTAAAGCTTGGGTGCTTAATGAGTGAGC 9225
QY 2369 TAACTCAATTAATTTGGTGGCTCACTCCCGCTTTCCAGTCGGGAACCTTCGTCG 2428
DB 9226 TAACTCAATTAATTTGGTGGCTCACTCCCGCTTTCCAGTCGGGAACCTTCGTCGTCG 9285
QY 2429 CAGCTGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2488
DB 9286 CAGCTGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 9345
QY 2489 TCCGCTTCTCGCTCACTCACTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 2548
DB 9346 TCCGCTTCTCGCTCACTCACTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 9405
QY 2549 GCTCACTCAAGCCGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2608
DB 9406 GCTCACTCAAGCCGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 9465
QY 2609 ATGTGAGCAAAAGGCCAGCAAGAACCGGTAAAGGCGCGCTTGTGTCGCTTT 2668
DB |||||

```
Db 9466 ATGTGAGCAAAAGGCGCAGCAAAAGGCGCAGCAAAAGGCGCGTTCGTCGCGTTT 9525
Qy 2669 TTCCATAGGCTCCGCCCCCTTGACGAGCATCAAAAATGACGCTCAAGTCAGAGTGG 2728
Db 9526 TTCCATAGGCTCCGCCCCCTTGACGAGCATCAAAAATGACGCTCAAGTCAGAGTGG 9585
Qy 2729 CGAAACCGCAGCAGACTATAAGATACCAAGCGCTTTCCCGCTGGAAGCTCCCTCGTCGC 2788
Db 9586 CGAAACCGCAGCAGACTATAAGATACCAAGCGCTTTCCCGCTGGAAGCTCCCTCGTCGC 9645
Qy 2789 TCTCCTGTTCGAACCTGCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGC 2848
Db 9646 TCTCCTGTTCGAACCTGCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGC 9705
Qy 2849 GTGGCGCTTCTCAATCTCAGCTGTAGGTATCTCAGTTTGGGTAGGTGCTTCGCTCC 2908
Db 9706 GTGGCGCTTCTCAATCTCAGCTGTAGGTATCTCAGTTTGGGTAGGTGCTTCGCTCC 9765
Qy 2909 AAGCTGGGCTGTGTGCAAGAACCCCGCTTCAGCCCGACCGCTCGCTTATCCGTTAAC 2968
Db 9766 AAGCTGGGCTGTGTGCAAGAACCCCGCTTCAGCCCGACCGCTCGCTTATCCGTTAAC 9825
Qy 2969 TATCGTCTTGAGTCAAAACCGGTTAAGACAGACTTATCGCACTTATCGCACTGGT 3028
Db 9826 TATCGTCTTGAGTCAAAACCGGTTAAGACAGACTTATCGCACTTATCGCACTGGT 9885
Qy 3029 AACAGGATACAGAGCGAGTATGTAGGCGGTCTACAGAGTCTTGAAGTGTGCGCT 3088
Db 9886 AACAGGATACAGAGCGAGTATGTAGGCGGTCTACAGAGTCTTGAAGTGTGCGCT 9945
Qy 3089 AACTACCGCTACACTAGAAGACAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTTACC 3148
Db 9946 AACTACCGCTACACTAGAAGACAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTTACC 10005
Qy 3149 TTGGAAGAAAGTGTGTAGCTTTGATCCGGCAAAACAAACCGCTGGTAGCGTGGT 3208
Db 10006 TTGGAAGAAAGTGTGTAGCTTTGATCCGGCAAAACAAACCGCTGGTAGCGTGGT 10065
Qy 3209 TTTTTCCTTTCAGCAGCAGATACCGCGAGAAAGGATCTCAAGAGATCTTTG 3268
Db 10066 TTTTTCCTTTCAGCAGCAGATACCGCGAGAAAGGATCTCAAGAGATCTTTG 10125
Qy 3269 ATCTTTTCTACGGGCTGTAGCTCAGTGGAAACGAAACTCAGCTTAAGGATTTGGTC 3328
Db 10126 ATCTTTTCTACGGGCTGTAGCTCAGTGGAAACGAAACTCAGCTTAAGGATTTGGTC 10185
Qy 3329 ATGAGCGGATACATATTTGAATGTATTAGA----- 3359
Db 10186 ATGAGATATCAAAAGGATCTTCACCTAGATCTTTTGGGTTGGCGCAAGAACTCCAGC 10245
Qy 3360 -----AAAATAACAAATAGGGTTCCGCGCACATTTCCCGCAAG 3401
Db 10246 ATGAGATCCCGCGCTGAGGATCATCAGCGCGGCTCCGGAAGAAAGATCCGAAAGCC 10305
Qy 3402 TGCCACCTGTATGCGGTG-----TGAATACCGCAGATCGTGAAGAGAAAT 3451
Db 10306 AACCTTTCTAAGAGCGCGGTGGAATCGAATCTGATGCGAGTTGGCGTCTGCT 10365
Qy 3452 ACCGATCAGGAATTTAAGCGTTAATAATACGAAGAATCTGCTCAAGAAAGCGATAGA 3511
Db 10366 TGGTCGGTCTATTCGAACCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAAGCGATAGA 10425
Qy 3512 AGCGATGCGCTCGAATCCGAGCGCGGATACGTTAAGCAGAGAGCGGTCCAGCC 3571
Db 10426 AGCGATGCGCTCGAATCCGAGCGCGGATACGTTAAGCAGAGAGCGGTCCAGCC 10485
Qy 3572 ATTCCGCGCAAGCTCTTCAGCAATATCAGGGTAGCCAGCTATGCTCTGATAGCGT 3631
Db 10486 ATTCCGCGCAAGCTCTTCAGCAATATCAGGGTAGCCAGCTATGCTCTGATAGCGT 10545
Qy 3632 CCGCCACCGCGCGCAGTCGATGAATCCAGAAAGCGGCGCATTTTCCACCATGA 3691
```

RESULT 12

US-09-861-101-2

; Sequence 2, Application US/09861101

; Publication No. US20030018984A1

; GENERAL INFORMATION:

; APPLICANT: COLEMAN, MICHAEL

; SCHWARTZ, ROBERT

; DEMAYO, FRANCESCO J.

; TITLE OF INVENTION: IGF-1 EXPRESSION SYSTEM AND

; METHODS OF USE

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: FastSeq for Windows 2.0

; CURRENT APPLICATION DATA:

/	APPLICATION NUMBER: US/09/861,101
/	FILING DATE: 18-May-2001
/	CLASSIFICATION: <Unknown>
/	PRIOR APPLICATION DATA:
/	APPLICATION NUMBER: 08/974,572
/	FILING DATE: November 19, 1997
/	APPLICATION NUMBER: 60/031,539
/	FILING DATE: December 2, 1996
/	ATTORNEY/AGENT INFORMATION:
/	NAME: Warburg, Richard J.
/	REGISTRATION NUMBER: 32,327
/	REFERENCE/DOCKET NUMBER: 230/185-PCT
/	TELECOMMUNICATION INFORMATION:
/	TELEPHONE: (213) 489-1600
/	TELEFAX: (213) 955-0440
/	TELEX: 67-3510
/	INFORMATION FOR SEQ ID NO: 2:
/	SEQUENCE CHARACTERISTICS:
/	LENGTH: 3600 base pairs
/	TYPE: nucleic acid
/	STRANDEDNESS: single
/	TOPOLOGY: linear
/	SEQUENCE DESCRIPTION: SEQ ID NO: 2:
/	US-09-861-101-2
Qy	Query Match 39.7%; Score 1719; DB 3; Length 3600;
Db	Best Local Similarity 90.8%; Pred. No. 0;
Qy	Matches 1923; Conservative 0; Mismatches 5; Indels 191; Gaps 1;
Db	
Qy	2214 CCAGCTTTTGTCCCTTTAGTGAGGGTTAAATTCGAGCTTGGCGTAATCATGTGCATAGC 2273
Db	20 CCAGCTTTTGTCCCTTTAGTGAGGGTTAAATTCGAGCTTGGCGTAATCATGTGCATAGC 79
Qy	2274 TGTTCCTGTGGAATTTGTTATCGCTCACAAATTCACACAACATAGAGCGGAAGCA 2333
Db	80 TGTTCCTGTGGAATTTGTTATCGCTCACAAATTCACACAACATAGAGCGGAAGCA 139
Qy	2334 TAAAGTGTAAAGCTCGGGTGTCTAATGAGTGAGCTAACTCACATTAATTCGTTGGCGT 2393
Db	140 TAAAGTGTAAAGCTCGGGTGTCTAATGAGTGAGCTAACTCACATTAATTCGTTGGCGT 199
Qy	2394 CACTGCCGCTTTCCAGTGGGAACCTGTGTGCGAGTGCAATTAATGAATCGGCCAAC 2453
Db	200 CACTGCCGCTTTCCAGTGGGAACCTGTGTGCGAGTGCAATTAATGAATCGGCCAAC 259
Qy	2454 GCSCGGGAGAGCGGTTTTGCGTATTGGCGCTCTTTCCGCTTCCTCGCTCACTGACTCGC 2513
Db	260 GCSCGGGAGAGCGGTTTTGCGTATTGGCGCTCTTTCCGCTTCCTCGCTCACTGACTCGC 319
Qy	2514 TGCGCTCGGTCGTTCCGCTGCGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGT 2573
Db	320 TGCGCTCGGTCGTTCCGCTGCGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGT 379
Qy	2574 TATCCACAGAATCAGGGGATACCGAGGAAGAACTGTGACAAAAGCCAGCAAAAGG 2633
Db	380 TATCCACAGAATCAGGGGATAACCGAGGAAGAACTGTGACAAAAGCCAGCAAAAGG 439
Qy	2634 CCAGGAACCTGAAAAAGGCGGTTGCTCGCGTTTTTCCATAGGCTTCGCCCCCTCGACG 2693
Db	440 CCAGGAACCTGAAAAAGGCGGTTGCTCGCGTTTTTCCATAGGCTTCGCCCCCTCGACG 499
Qy	2694 AGCATCAAAAAATTCAGCGCTCAAGTTCAGAGTGGCGAAACCCGACAGGACTATAAGAT 2753
Db	500 AGCATCAAAAAATTCAGCGCTCAAGTTCAGAGTGGCGAAACCCGACAGGACTATAAGAT 559
Qy	2754 ACCAGGCGTTTTCCCCTTGAAGCTCCCTGTGCGGCTCTCTGTTCCGACCCTGCGCGCTTA 2813
Db	560 ACCAGGCGTTTTCCCCTTGAAGCTCCCTGTGCGGCTCTCTGTTCCGACCCTGCGCGCTTA 619
Qy	2814 CCGGATACCTGTCCGCTTTTCTCCCTTCGGGAAGCGTGGCGTTTCTCAATGCTCACGCT 2873
Db	620 CCGGATACCTGTCCGCTTTTCTCCCTTCGGGAAGCGTGGCGTTTCTCAATGCTCACGCT 679


```

Db      1569  AGCAAGGTGAGATGACAGGAGATCTGCGCGGCACTTGGCCCAATAGCAGCCAGTCCCT 1628
Qy      4014  TCCCGCTTCAGTGCACAGCTGCAGCAGCTGCCAAGGACGCCCTGTCGTCAGCCCA 4073
Db      1629  TCCCGCTTCAGTGCACAGCTGCAGCAGCTGCCAAGGACGCCCTGTCGTCAGCCCA 1688
Qy      4074  CGATAGCGCGCTCGCTCGCTTTCAGTTCATTCAGGCGCACCGGACAGCTCGGTCCTGAC 4133
Db      1689  CGATAGCGCGCTCGCTCGCTTTCAGTTCATTCAGGCGCACCGGACAGCTCGGTCCTGAC 1748
Qy      4134  AAAAAGAACCGGGCGCCCTGCGCTGCAGCGGAAACAGCGCGCATCAGAGCGCGAT 4193
Db      1749  AAAAAGAACCGGGCGCCCTGCGCTGCAGCGGAAACAGCGCGCATCAGAGCGCGAT 1808
Qy      4194  TGTCTGTTGTGCCAGTCATAGCGGATAGCTCTCCACCCAGCGCGCGGAGAACCTGC 4253
Db      1809  TGTCTGTTGTGCCAGTCATAGCGGATAGCTCTCCACCCAGCGCGCGGAGAACCTGC 1868
Qy      4254  GTGCAATCCATCTTGTTCATCATCGGAAACGATCCTCATCTGCTCTTGTATCAGAGCT 4313
Db      1869  GTGCAATCCATCTTGTTCATCATCGGAAACGATCCTCATCTGCTCTTGTATCAGATCT 1928
Qy      4314  TGATCCCTCGGCCATCAG 4332
Db      1929  TGATCCCTCGGCCATCAG 1947

```

RESULT 13

```

US-10-021-403A-10
; Sequence 10, Application US/10021403A
; Publication No. US20030074679A1
; GENERAL INFORMATION:
; APPLICANT: Adviseys
; TITLE OF INVENTION: Administration of Nucleic Acid Sequence to Female Animal to Enhance
; TITLE OF INVENTION: Growth in Offspring
; FILE REFERENCE: HO-P02021US1/100021476/OTA 00-91
; CURRENT APPLICATION NUMBER: US/10/021.403A
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/255,021
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; LENGTH: 2192
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: This is a plasmid vector comprising a pVC0289 backbone
US-10-021-403A-10

```

```

Query Match      39.78; Score 1718.4; DB 5; Length 2192;
Best Local Similarity 90.58; Pred. No. 0;
Matches 1926; Conservative 0; Mismatches 11; Indels 191; Gaps 1;

; Qy      2205  GCCACAGCTCCAGCTTTGTTTCCCTTTAGTGAGGGTTAAATTCGAGCTTGGCGTAATCAT 2264
Db      24      GGCCCGGTACCAGCTTTGTTTCCCTTTAGTGAGGGTTAAATTCGAGCTTGGCGTAATCAT 83
Qy      2265  GGTCTATAGCTGTTTCCCTGTTGTAATTTGTTATCCGCTCACATTCACACACATACGAG 2324
Db      84      GGTCTATAGCTGTTTCCCTGTTGTAATTTGTTATCCGCTCACATTCACACACATACGAG 143
Qy      2325  CCGGAAGCATAAAGTGTAAAGCTTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTG 2384
Db      144      CCGGAAGCATAAAGTGTAAAGCTTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTG 203
Qy      2385  CGTTGCGCTCACTGCCCGCTTTTCAGTCCGGAACCTGTGTCAGCTGCATTAATGAA 2444
Db      204      CGTTGCGCTCACTGCCCGCTTTTCAGTCCGGAACCTGTGTCAGCTGCATTAATGAA 263
Qy      2445  TCGGCCAACCGCGGGAGAGGGGTTTGGTATTGGGCGCTCTTCGCTTCCCTCGCTCA 2504

```

```

264  TCGGCCAAACGCGCGGGAGAGCGGTTTGGCTATTGGGCGCTCTTCCGCTTCTCGCTCA 323
2505  CTGACTCGCTGCGCTCGGTCGTTGGCTGCGGCGAGCGGTATCAGCTCACTCAAGAGCGG 2564
324  CTGACTCGCTGCGCTCGGTCGTTGGCTGCGGCGAGCGGTATCAGCTCACTCAAGAGCGG 383
2565  TAATAAGCGTTATCCACAGAATCAGGGGATAACCGAGGAAAGAACATGTGAGCAAAAGGCC 2624
384  TAATAAGCGTTATCCACAGAATCAGGGGATAACCGAGGAAAGAACATGTGAGCAAAAGGCC 443
2625  AGCAAAAGGCCAGGAAACCGTAAAGAGCGCTGCTGGCGTTTTCATAGGCTCGGCC 2684
444  AGCAAAAGGCCAGGAAACCGTAAAGAGCGCTGCTGGCGTTTTCATAGGCTCGGCC 503
2685  CCCCTGACGAGCATCACAAAATCGAGCTCAAGTCAGAGGTGGCGAAACCCGACAGGAC 2744
504  CCCCTGACGAGCATCACAAAATCGAGCTCAAGTCAGAGGTGGCGAAACCCGACAGGAC 563
2745  TATAAAGATACCAAGGCGTTTCCCGCTGGAAAGCTCCCTCGTGGCTCTCTGTTCCGACCC 2804
564  TATAAAGATACCAAGGCGTTTCCCGCTGGAAAGCTCCCTCGTGGCTCTCTGTTCCGACCC 623
2805  TGGCGCTTACCGGATACCTGTCGCGCTTCTCCCTCGGGAAGCGTGGCGCTTCTCAAT 2864
624  TGGCGCTTACCGGATACCTGTCGCGCTTCTCCCTCGGGAAGCGTGGCGCTTCTCAT 683
2865  GCTCAGCTGTAGTATCTCAGTTCGCTGAGTGTGCTTCCCTCGGGAAGCGTGGCGCTGTC 2924
684  GCTCAGCTGTAGTATCTCAGTTCGCTGAGTGTGCTTCCCTCGGGAAGCGTGGCGCTGTC 743
2925  ACGAAACCCCGCTTACGCGCGACCGCTGCGCTTATCCGCTAACTATCGTCTTGAGTCCA 2984
744  ACGAAACCCCGCTTACGCGCGACCGCTGCGCTTATCCGCTAACTATCGTCTTGAGTCCA 803
2985  ACCCGGTAGACACGAGCTTATCCCGCTGCGAGCGCTTATCCGCTAACTATCGTCTTGAGTCCA 3044
804  ACCCGGTAGACACGAGCTTATCCCGCTGCGAGCGCTTATCCGCTAACTATCGTCTTGAGTCCA 863
3045  CGAGGTATGTAGCGGTGTCTACAGAGTTCCTTGAAGTGGTGGCTTAACTACGGCTTACACTA 3104
864  CGAGGTATGTAGCGGTGTCTACAGAGTTCCTTGAAGTGGTGGCTTAACTACGGCTTACACTA 923
3105  GAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAAAGAGTTG 3164
924  GAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAAAGAGTTG 983
3165  GTAGCTCTTGATCCGCAACAAACCCGCTGCTGAGCGGTGTTTGTGTTGCAAGC 3224
984  GTAGCTCTTGATCCGCAACAAACCCGCTGCTGAGCGGTGTTTGTGTTGCAAGC 1043
3225  AGCAGATTACGCGCAGAAAAAGGATCTCAAGAGATCTTTGATCTTTTCTACGGGT 3284
1044  AGCAGATTACGCGCAGAAAAAGGATCTCAAGAGATCTTTGATCTTTTCTACGGGT 1103
3285  CTGACGCTCAGTGGAAACGAAACTCAGTTAAGGATTTTGGTCATGAGCGGATACATAT 3344
1104  CTGACGCTCAGTGGAAACGAAACTCAGTTAAGGATTTTGGTCATGAGCGGATACATAT 1110
3345  TTGAATGTATTAGAAAAATAAACAATAGGGGTTCCGCGCACATTTCCCGGAAAGTGC 3404
1111  TTGAATGTATTAGAAAAATAAACAATAGGGGTTCCGCGCACATTTCCCGGAAAGTGC 1110
3405  CACCTGTATGCGGTGTGAATAATCCGACAGATCGCTAAGGAGAAAAATACCGCATCAGAA 3464
1111  CACCTGTATGCGGTGTGAATAATCCGACAGATCGCTAAGGAGAAAAATACCGCATCAGAA 1110
3465  ATTGTAAGCGTTAATATTCAAGAAAGCTCGTCAAGAGCGATAGAGCGGATGCGCTG 3524
1111  ATTGTAAGCGTTAATATTCAAGAAAGCTCGTCAAGAGCGATAGAGCGGATGCGCTG 1152
3525  CGAATCGGAGCGCGATACCGGTAAAGCAGAGGAGCGGTACGCCATTTCCGCGCCAAAG 3584
1153  CGAATCGGAGCGCGATACCGGTAAAGCAGAGGAGCGGTACGCCATTTCCGCGCCAAAG 1212

```



```
QY 3585 CTCTTACGCAATATACGGGTAGCAACGCTATGTCTGTATAGCGGTCCGCCACACCCAG 3644
Db 1213 CTCTTACGCAATATACGGGTAGCAACGCTATGTCTGTATAGCGGTCCGCCACACCCAG 1272
QY 3645 CCGGCCACAGTCGATGATCCAGAAAGCGGCCATTTTCCACCATGATATTCGSCAAGCA 3704
Db 1273 CCGGCCACAGTCGATGATCCAGAAAGCGGCCATTTTCCACCATGATATTCGSCAAGCA 1332
QY 3705 GGCATCGCATGGGTACAGACGAGATCCTCCCGTCCGGCATGTCTCGCTTGGAGCTGGC 3764
Db 1333 GGCATCGCATGGGTACAGACGAGATCCTCCCGTCCGGCATGTCTCGCTTGGAGCTGGC 1392
QY 3765 GAAACAGTTCCGCTGGCGAGCCCTGATGCTCTTCTGTCAGATCATCTCTGATCGACAAG 3824
Db 1393 GAAACAGTTCCGCTGGCGAGCCCTGATGCTCTTCTGTCAGATCATCTCTGATCGACAAG 1452
QY 3825 ACCGGCTTCCATCCGAGTACGTCTCGCTCGATCGGATGTTTCGCTTGGTGGTGGATGG 3884
Db 1453 ACCGGCTTCCATCCGAGTACGTCTCGCTCGATCGGATGTTTCGCTTGGTGGTGGATGG 1512
QY 3885 GCAGTACCCGATCAACCGTATGACGCGCGCATTCATCAGCCATGATGGATACCTT 3944
Db 1513 GCAGTACCCGATCAACCGTATGACGCGCGCATTCATCAGCCATGATGGATACCTT 1572
QY 3945 CTCGGCAGGACAGGTGAGATGACAGAGATCTCTGCCCCGGCATCTCGCCCAATAGCAG 4004
Db 1573 CTCGGCAGGACAGGTGAGATGACAGAGATCTCTGCCCCGGCATCTCGCCCAATAGCAG 1632
QY 4005 CCAGTCCCTTCCCGTTCAGTGACAACTCGAGACAGCTCGGAGAAAGCGCGTCTGT 4064
Db 1633 CCAGTCCCTTCCCGTTCAGTGACAACTCGAGACAGCTCGGAGAAAGCGCGTCTGT 1692
QY 4065 GSCCAGGACAGATAGCCGCTGCTCTGTCAGATTCATTCAGGGCACCGGACAGGTC 4124
Db 1693 GSCCAGGACAGATAGCCGCTGCTCTGTCAGATTCATTCAGGGCACCGGACAGGTC 1752
QY 4125 GGTCTTGAACAAAGAACCGGGCGCCCTGCGCTGACAGCGGAAACACGGGGCATCAGA 4184
Db 1753 GGTCTTGAACAAAGAACCGGGCGCCCTGCGCTGACAGCGGAAACACGGGGCATCAGA 1812
QY 4185 GCAGCGGATGTCTGTGCGCCAGTCATAGCGAATAGCCTCTCCACCCAGCGGCGCG 4244
Db 1813 GCAGCGGATGTCTGTGCGCCAGTCATAGCGAATAGCCTCTCCACCCAGCGGCGCG 1872
QY 4245 AGAACCTGCGTCAATCCATCTTGTTCATCATGCGAAACGATCCTCATCTCTCTTG 4304
Db 1873 AGAACCTGCGTCAATCCATCTTGTTCATCATGCGAAACGATCCTCATCTCTCTTG 1932
QY 4305 ATCAGAGCTTGATCCCTGCGCCATCAG 4332
Db 1933 ATCAGAGCTTGATCCCTGCGCCATCAG 1960
```

```
RESULT 14
US-10-136-837-2
; Sequence 2, Application US/10136837
; Publication No. US20030181405A1
; GENERAL INFORMATION:
; APPLICANT: NORDSTROM, Jeffrey L
; APPLICANT: PERICLE, Federica
; APPLICANT: ROLLAND, Alain
; APPLICANT: RALSTON, Robert
; TITLE OF INVENTION: Interferon Alpha Plasmids and Delivery Systems, and Methods of Ma
; TITLE OF INVENTION: Using the Same
; FILE REFERENCE: 273/082 (GM15-1USC1)
; CURRENT APPLICATION NUMBER: US/10/136,837
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 09/268,135
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
```

```
; LENGTH: 3426
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mouse Interferon Alpha pIF0826
US-10-136-837-2

Query Match 39.7%; Score 1718.4; DB 6; Length 3426;
Best Local Similarity 90.5%; Pred. No. 0;
Matches 1926; Conservative 0; Mismatches 11; Indels 191; Gaps 1;

QY 2205 GCCACAGCTCCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTTTCGAGCTTGGCGTAATCAT 2264
Db 793 GGCCTGGTACAGCTTTTGTTCCTTTAGTGAGGGTTAAATTTTCGAGCTTGGCGTAATCAT 852
QY 2265 GGTTCATAGCTTTTTCCTGTGTGAAATTTTATCCGCTCACAATTTCCACACAATACGAG 2324
Db 853 GGTTCATAGCTTTTTCCTGTGTGAAATTTTATCCGCTCACAATTTCCACACAATACGAG 912
QY 2325 CCGAAGCATAAAGTGTAAAGCTTGGGGTGCCTAATGAGTGCAGCTAATCACTCAATTAATG 2384
Db 913 CCGAAGCATAAAGTGTAAAGCTTGGGGTGCCTAATGAGTGCAGCTAATCACTCAATTAATG 972
QY 2385 GGTTCGCTCACTCCCGCTTTCCAGTCGGGAAACCTGTCTGTCGAGCTGCATTAATGAA 2444
Db 973 GGTTCGCTCACTCCCGCTTTCCAGTCGGGAAACCTGTCTGTCGAGCTGCATTAATGAA 1032
QY 2445 TCGGCCAAACGCGCGGGGAGAGCGGTTTGTCTATTTGGGCGCTCTTCCGCTTCTCGCTCA 2504
Db 1033 TCGGCCAAACGCGCGGGGAGAGCGGTTTGTCTATTTGGGCGCTCTTCCGCTTCTCGCTCA 1092
QY 2505 CTGACTCGCTCGCTCGCTCGCTTCCGCTGCGGCGAGGATCAGCTCACTCAAGAGCGG 2564
Db 1093 CTGACTCGCTCGCTCGCTCGCTTCCGCTGCGGCGAGGCGGTATCAGCTCACTCAAGAGCGG 1152
QY 2565 TAATACGCTTATCCACAGAAATCAGGGGATACCGAGGAAAGAAACATGTGAGCAAAAGGCC 2624
Db 1153 TAATACGCTTATCCACAGAAATCAGGGGATACCGAGGAAAGAAACATGTGAGCAAAAGGCC 1212
QY 2625 AGCAAAAGGCGAGGAAACCGTAAAAAGCGCGTGTCTGGCGTTTTCATAGGCTCCGCG 2684
Db 1213 AGCAAAAGGCGAGGAAACCGTAAAAAGCGCGTGTCTGGCGTTTTCATAGGCTCCGCG 1272
QY 2685 CCCCTGACGAGCATCACAAAATCAGCCCTCAAGTCAGAGTGGCGAAACCCGACAGGAC 2744
Db 1273 CCCCTGACGAGCATCACAAAATCAGCCCTCAAGTCAGAGTGGCGAAACCCGACAGGAC 1332
QY 2745 TATAAAGATACAGGCGGTTTCCCTCTGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCC 2804
Db 1333 TATAAAGATACAGGCGGTTTCCCTCTGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCC 1392
QY 2805 TGCCGCTTACCGGATACCTGTCCGCTTTCCTTCCGGAAGCGTGGGCTTCTCAAT 2864
Db 1393 TGCCGCTTACCGGATACCTGTCCGCTTTCCTTCCGGAAGCGTGGGCTTCTCAAT 1452
QY 2865 GCTCAGCTGTAGGTATCTCAGTTCGCTGTAGTGTCTGCTCCAGCTGGGCTGTGTGC 2924
Db 1453 GCTCAGCTGTAGGTATCTCAGTTCGCTGTAGTGTCTGCTCCAGCTGGGCTGTGTGC 1512
QY 2925 ACGAAACCCCGCTTCCAGCCCGACCGCTGCGCTTATCCGGTAACTATCGTCTGTAGTCCA 2984
Db 1513 ACGAAACCCCGCTTCCAGCCCGACCGCTGCGCTTATCCGGTAACTATCGTCTGTAGTCCA 1572
QY 2985 ACCCGGTAAAGACACACTTATCCGCACTGGCAGAGCCACTGTGTACAGGATAGCAGAG 3044
Db 1573 ACCCGGTAAAGACACACTTATCCGCACTGGCAGAGCCACTGTGTGTACAGGATAGCAGAG 1632
QY 3045 CGAGGTATGTAGCGGTGCTACAGAGTCTTCAAGTGTGTGGCTTAACCTACGGCTACACTA 3104
Db 1633 CGAGGTATGTAGCGGTGCTACAGAGTCTTCAAGTGTGTGGCTTAACCTACGGCTACACTA 1692
QY 3105 GAAGGACAGTATTTGGTATCTCGCTGCTGAGGCGAGTTCCTTCCGAAAAAGAGTTG 3164
```

D	b	1693	GAAGGACAGTATTGTGGTATCTGCGGCTGTGCTGAAGCCAGTTACCTTCGGAAAAAAGAGTTG	1751
Q	y	3165	GTAGCTCTTGATCGGCAAAACAAACCACCGCTGCTAGCGGTGGTTTTTTTGTGTTTGCAGC	3224
D	b	1753	GTAGCTCTTGATCGGCAAAACAAACCACCGCTGCTAGCGGTGGTTTTTTTGTGTTGCAAGC	1812
Q	y	3225	AGCAGATTACGCCGACAGAAAAAGGATCTCAAGAAGATCTCTTTGATCTTTCTACGGGGT	3284
D	b	1813	AGCAGATTACGCCGACAGAAAAAGGATCTCAAGAAGATCTCTTTGATCTTTCTACGGGGT	1872
Q	y	3285	CTGACGCTCAGTGGAAAGAAAACACTCACGTTAAGGATTTTGGTCTATGAGCGGATACATAT	3344
D	b	1873	CTGACG-----	1879
Q	y	3345	TTGAATGTATTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCGAAAAAGTGC	3404
D	b	1880	-----	1879
Q	y	3405	CACCTGTATGCGGTGTGAATACCGCACAGATGCGTAAGGAGAAAAATACCGCATCAGGAA	3464
D	b	1880	-----	1879
Q	y	3465	ATTGTAAGCGTTAATAATTCAGAGAAGTCTGTCAAGAGCGGATAGAAAGCGGATGCGCTG	3524
D	b	1880	-----TCAGAAGAAGTCTGTCAAGAGGCGATAGAAAGCGGATGCGCTG	1921
Q	y	3525	CGAATCGGAGCGCGGATACCGTAAAGCACAGGAAGCGGTTCAGCCCATTTCCGCCCAAG	3584
D	b	1922	CGAATCGGAGCGCGGATACCGTAAAGCACAGGAAGCGGTTCAGCCCATTTCCGCCCAAG	1981
Q	y	3585	CTCTTTAGCAATATCA CGGGTAGCCAACGCTATCTCTGATAGCGGTCCGCCACACCCAG	3644
D	b	1982	CTCTTTAGCAATATCACGGGTAGCCAACGCTATCTCTGATAGCGGTCCGCCACACCCAG	2041
Q	y	3645	CCGCCACAGTCGATGTAATCCAGAAAGCGGCCATTTCCACCATGATATTGGCAAGCA	3704
D	b	2042	CCGCCACAGTCGATGTAATCCAGAAAGCGGCCATTTTCACCATGATATTGGCAAGCA	2101
Q	y	3705	GGCATCGCCATGGGTCAAGCAGAGATCCTCGCCGTCGGGGATGCTCGCCTTGAGCCCTGGC	3764
D	b	2102	GGCATCGCCATGGGTCAAGCAGAGATCCTCGCCGTCGGGGATGCTCGCCTTGAGCCCTGGC	2161
Q	y	3765	GAAACAGTTTCGGCTGGCGGAGCCCTGATGCTTTGCTCAGATCATCTCTGATCGACAAG	3824
D	b	2162	GAAACAGTTTCGGCTGGCGGAGCCCTGATGCTTTGCTCAGATCATCTCTGATCGACAAG	2221
Q	y	3825	ACCGGCTTCCATCCGAGTACGTGCTCCTCGATCGAGTGTTCGTTGGTGGTCAATGG	3884
D	b	2222	ACCGGCTTCCATCCGAGTACGTGCTCCTCGATCGAGTGTTCGTTGGTGGTCAATGG	2281
Q	y	3885	GCAGTAGCCGATCAAGCGTATGACGCCCGCATTTGCATCAGCCATGATGATATCTTT	3944
D	b	2282	GCAGTAGCCGATCAAGCGTATGACGCCCGCATTTGCATCAGCCATGATGATATCTTT	2341
Q	y	3945	CTCGCAGGAGCAAGGTGAGATGACAGGAGATCTCGCCCGGCACCTTCGCCCAATAGCAG	4004
D	b	2342	CTCGCAGGAGCAAGGTGAGATGACAGGAGATCTCGCCCGGCACCTTCGCCCAATAGCAG	2401
Q	y	4005	CCAGTCTCTTCCGCTTCAGTGAACAGTTCGAGCACAGTTCGGAAGGAACGCCGTCGT	4064
D	b	2402	CCAGTCTCTTCCGCTTCAGTGAACAGTTCGAGCACAGTTCGGAAGGAACGCCGTCGT	2461
Q	y	4065	GGCCAGCACGATAGCCGCTGCTCTTGAGTTCATTCAGGSCACCGGACAGGTC	4124
D	b	2462	GGCCAGCACGATAGCCGCTGCTCTTGAGTTCATTCAGGSCACCGGACAGGTC	2521
Q	y	4125	GGTCTTGACAAAAAGAACCGGGGCCCCCTGCTGTGACAGCCGGAACACGGCGGCATCAGA	4184
D	b	2522	GGTCTTGACAAAAAGAACCGGGGCCCCCTGCTGTGACAGCCGGAACACGGCGGCATCAGA	2581
Q	y	4185	GCAGCCGATTTGTTGTGCCGCTCATAGCCGATPAGCTCTCCACCAAGCGGCGCG	4244
D	b	2582	GCAGCCGATTTGTTGTGCCGCTCATAGCCGATPAGCTCTCCACCAAGCGGCGCG	2641

Qy	4245	AGAACCTGCGTGC	AAATCACTTTGTTCAATCATCGCGAAA	CGATCCTCATCTGTCCTTGTG	4304
Db	2642	AGAACCTGCGTGC	AAATCACTTTGTTCAATCATCGCGAAA	CGATCCTCATCTGTCCTTGTG	2701
Qy	4305	ATCAGAGCTTGAT	CCCCCTGCGCCATCAG		4332
Db	2702	ATCAGATCTTGAT	CCCCCTGCGCCATCAG		2729

RESULT 15

```

US-10-021-403A-9
; Sequence 9, Application US/10021403A
; Publication No. US20030074679A1
; GENERAL INFORMATION:
; APPLICANT: Advisys
; TITLE OF INVENTION: Administration of Nucleic Acid Sequence to Female Animal to Enhance
; TITLE OF INVENTION: Growth in Offspring
; FILE REFERENCE: HO-P02021US1/100021476/OTA 00-91
; CURRENT APPLICATION NUMBER: US/10/021.403A
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/255,021
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: This is a plasmid pSPC5-12-HVGHRR utilized in the present invention
; OTHER INFORMATION: on.
US-10-021-403A-9

```

Query Match 39.7%; Score 1718.4; DB 5; Length 3534;
Best Local Similarity 90.5%; Pred. No. 0;
Matches 1926; Conservative 0; Mismatches 11; Indels 191; Gaps 1;

Qy	2205	GCACAGCTCCAGCTTTTGTTCCGTTTGTAGTGAGGGTTAAATTTTCGAGCTTCGGCGTAATCAT	2264
Db	1366	GGCCCGGTACACGCTTTTGTTCCTTTTGTAGTGAGGGTTAAATTTTCGAGCTTCGGCGTAATCAT	1425
Qy	2265	GGTCATAGCTGTTTCCGTGTGAAATTTGTTATCCGCTCACAATTCACACAAACATACGAG	2324
Db	1426	GGTCATAGCTGTTTCCGTGTGAAATTTGTTATCCGCTCACAATTCACACAAACATACGAG	1485
Qy	2325	CCGGAAGCATAAAGTGTAAGAGCTCGGGTGCCCTAAATGAGTGAGCTAACTCACATTTAATTG	2384
Db	1486	CCGGAAGCATAAAGTGTAAGAGCTCGGGTGCCCTAAATGAGTGAGCTAACTCACATTTAATTG	1545
Qy	2385	CGTTGCGCTCACATGCCCGCTTCCAGTTCGGGAAACCTGTCGCCAGCTGCATTAATGAA	2444
Db	1546	CGTTGCGCTCACATGCCCGCTTCCAGTTCGGGAAACCTGTCGCCAGCTGCATTAATGAA	1605
Qy	2445	TCGGCCAAACCGCGGGGAGAGCGGTTTCGTTATTCGGGCGCTCTTCGCGTTTCCCTGCTCA	2504
Db	1606	TCGGCCAAACCGCGGGGAGAGCGGTTTCGTTATTCGGGCGCTCTTCGCGTTTCCCTGCTCA	1665
Qy	2505	CTGACTCGCTCGCTCGGTCGCTGCGCGCGGAGCGGTATCAGCTCAGCTCAAGAGCGG	2564
Db	1666	CTGACTCGCTCGCTCGGTCGCTGCGCGCGGAGCGGTATCAGCTCAGCTCAAGAGCGG	1725
Qy	2565	TAATACGGTTTATCCACAGAATCAGGGGATAACCGCAGGAAGAAACATGTGAGCAAAAGGCC	2624
Db	1726	TAATACGGTTTATCCACAGAATCAGGGGATAACCGCAGGAAGAAACATGTGAGCAAAAGGCC	1785
Qy	2625	AGCAAAAGGCCAGAACCGGTAAAGAGCCGCTGCTGGCGTTTTTCCATAGAGCTCCGCC	2684
Db	1786	AGCAAAAGGCCAGAACCGGTAAAGAGCCGCTGCTGGCGTTTTTCCATAGAGCTCCGCC	1845
Qy	2685	CCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGGAAACCCGACAGGAC	2744
Db	1846	CCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGGAAACCCGACAGGAC	1905

Qy 2745 TATAAGATACCGCGTTTCCCTCGTGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCC 2804
Db |||||
Qy 1906 TATAAGATACCGCGGTTTCCCTCGTGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCC 1965
Db |||||
Qy 2805 TGCCGCTTACCGGATACCTGTCCGCTTTCCTTCGGGAAGCGTGGCGCTTCTCAAT 2864
Db |||||
Qy 1966 TGCCGCTTACCGGATACCTGTCCGCTTTCCTTCGGGAAGCGTGGCGCTTCTCAT 2025
Db |||||
Qy 2865 GCTCAGCGTAGGTATCTCAGTTCGGGTAGGTTCGCTCCCAAGCTGGCGTGTGTC 2924
Db |||||
Qy 2026 GCTCAGCGTAGGTATCTCAGTTCGGGTAGGTTCGCTCCCAAGCTGGCGTGTGTC 2085
Db |||||
Qy 2925 ACGAACCCCGCTTCAGCGCCAGCGCTTCGCTTATCCGGTAACTATCGTCTTCAGTCCA 2984
Db |||||
Qy 2086 ACGAACCCCGCTTCAGCGCCAGCGCTTCGCTTATCCGGTAACTATCGTCTTCAGTCCA 2145
Db |||||
Qy 2985 ACCCGTTAAGACACGACTTATCGGCACTGGGAGCGGCACTGGTAAACGAGATTAGCAGAG 3044
Db |||||
Qy 2146 ACCCGTTAAGACACGACTTATCGGCACTGGGAGCGGCACTGGTAAACGAGATTAGCAGAG 2205
Db |||||
Qy 3045 CGAGGTATGTAAGCGGTCTACAGAGTTCCTGAAGTGGTGGCTTAACTACGCGTACACTA 3104
Db |||||
Qy 2206 CGAGGTATGTAAGCGGTCTACAGAGTTCCTGAAGTGGTGGCTTAACTACGCGTACACTA 2265
Db |||||
Qy 3105 GAAGGACAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTG 3164
Db |||||
Qy 2266 GAAGAACAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTG 2325
Db |||||
Qy 3165 GTAGCTCTTGATTCGGGCAAAACAAACACCGCTGGTAGCGGTGTTTTTTGTTTGCAGGC 3224
Db |||||
Qy 2326 GTAGCTCTTGATTCGGGCAAAACAAACACCGCTGGTAGCGGTGTTTTTTGTTTGCAGGC 2385
Db |||||
Qy 3225 AGCAGATTACGGCGAGAAAAAAGGATCTCAAGAGATCCTTTTGATCTTTCTACGGGT 3284
Db |||||
Qy 2386 AGCAGATTACGGCGAGAAAAAAGGATCTCAAGAGATCCTTTTGATCTTTCTACGGGT 2445
Db |||||
Qy 3285 CTGACGCTCAGTGGAAACGAAACTCACGTTAAGGGATTTTGGTCATGAGCGGATACATAT 3344
Db |||||
Qy 2446 CTGACGC----- 2452
Db |||||
Qy 3345 TTGAATGATTTAGAAAAATAAAATAAGGGTTCCGGGCACATTTCCCGAAAAAGTGC 3404
Db |||||
Qy 2453 ----- 2452
Db |||||
Qy 3405 CACCTGTATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAAATACCGCATCAGGAA 3464
Db |||||
Qy 2453 ----- 2452
Db |||||
Qy 3465 ATTGTAAGCGTTAATAATTCAAGAAACCTCGTCAAGAAAGCGGATAGAGCGGATCGGCTG 3524
Db |||||
Qy 2453 -----TCAGAAAGAACTCGTCAAGAGGCGATAGAGGCGGATCGGCTG 2494
Db |||||
Qy 3525 CGAATCGGAGCGGCGATACCGTAAAGCACGAGGAGCGGTTCAGCCCATTCGCCGCCAAG 3584
Db |||||
Qy 2495 CGAATCGGAGCGGCGGATACCGTAAAGCACGAGGAGCGGTTCAGCCCATTCGCCGCCAAG 2554
Db |||||
Qy 3585 CTCTTCAGCAATATACCGGTAGCCAAACGCTATGCTCTGATAGCGGTTCGCCACACCCAG 3644
Db |||||
Qy 2555 CTCTTCAGCAATATACCGGTAGCCAAACGCTATGCTCTGATAGCGGTTCGCCACACCCAG 2614
Db |||||
Qy 3645 CCGGCCACAGTCGATGAATCCAGAAAGCGGCAATTTTCCACATGATATTCGGCAAGCA 3704
Db |||||
Qy 2615 CCGGCCACAGTCGATGAATCCAGAAAGCGGCAATTTTCCACATGATATTCGGCAAGCA 2674
Db |||||
Qy 3705 GGCATCGCCATGGGTTCAGACGAGATCCTCGCGTCGGGCATGCTCGCTTGAGCCTGSC 3764
Db |||||
Qy 2675 GGCATCGCCATGGGTTCAGACGAGATCCTCGCGTCGGGCATGCGGCGCTTGAGCCTGSC 2734
Db |||||
Qy 3765 GAACAGTTCCGCTGGCGCGAGCCCTGATGCTCTCTGTCAGATCATCTGATCGACAAG 3824
Db |||||
Qy 2735 GAACAGTTCCGCTGGCGCGAGCCCTGATGCTCTCTGTCAGATCATCTGATCGACAAG 2794
Db |||||

Qy 3825 ACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTGAATGG 3884
Db |||||
Qy 2795 ACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTGAATGG 2854
Db |||||
Qy 3885 GCAGGTAGCGGATCAAGCGTATGACGCGCGCATTTGCATCAGCCATGATGATGATCTTT 3944
Db |||||
Qy 2855 GCAGGTAGCGGATCAAGCGTATGACGCGCGCATTTGCATCAGCCATGATGATGATCTTT 2914
Db |||||
Qy 3945 CTGGCAGGAGCAAGGTGAGATGACAGGAGATCTGCCCCGGCACTTTCGCCCAATAGCAG 4004
Db |||||
Qy 2915 CTGGCAGGAGCAAGGTGAGATGACAGGAGATCTGCCCCGGCACTTTCGCCCAATAGCAG 2974
Db |||||
Qy 4005 CCAGTCCCTTCCCGCTTCAGTGACAAAGTTCAGGACAGCTGCGCAAGGAAAGCGCCGCT 4064
Db |||||
Qy 2975 CCAGTCCCTTCCCGCTTCAGTGACAAAGTTCAGGACAGCTGCGCAAGGAAAGCGCCGCT 3034
Db |||||
Qy 4065 GGCCAGCCACGATAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4124
Db |||||
Qy 3035 GGCCAGCCACGATAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3094
Db |||||
Qy 4125 GGTCTTGACAAAAAGAAACCGGGCGCCCTGCGCTGACAGCGGGAACACGCGGCGCATCAGA 4184
Db |||||
Qy 3095 GGTCTTGACAAAAAGAAACCGGGCGCCCTGCGCTGACAGCGGGAACACGCGGCGCATCAGA 3154
Db |||||
Qy 4185 GCAGCCGATTTGCTGTTGTTGCGCCAGTATAGCCGATAGCTCTCCACCCAAAGCGGCGG 4244
Db |||||
Qy 3155 GCAGCCGATTTGCTGTTGTTGCGCCAGTATAGCCGATAGCTCTCCACCCAAAGCGGCGG 3214
Db |||||
Qy 4245 AGAACCTGCGTGCAATCCATCTTCTCAATCATCGGAAACGATCCTCATCTGCTCTTTG 4304
Db |||||
Qy 3215 AGAACCTGCGTGCAATCCATCTTCTCAATCATCGGAAACGATCCTCATCTGCTCTTTG 3274
Db |||||
Qy 4305 ATCAGAGCTTGATCCCTCGGCCATCAG 4332
Db |||||
Qy 3275 ATCAGATCTTGATCCCTCGGCCATCAG 3302
Db |||||

Search completed: March 15, 2006, 21:00:20
Job time : 3019 secs

November 2005

Published_Applications_Nucleic Acid and Published_Applications_Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

This Page Blank (uspto)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2006, 20:54:32 ; Search time 1189 Seconds
(without alignments)
8495.331 Million cell updates/sec

Title: US-10-811-028A-1

Perfect score: 4331

Sequence: 1 cggcggggctcttcgcta.....ttgatccctgcgcattcag 4332

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 8023312 seqs, 1165852854 residues

Total number of hits satisfying chosen parameters: 16046624

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications NA New:
- 1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:
 - 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
 - 3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
 - 4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
 - 5: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq:
 - 6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
 - 7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
 - 8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
 - 9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
 - 10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
 - 11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
 - 12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
 - 13: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1718.4	39.7	3534	7	US-10-764-818A-11
2	1718.4	39.7	3534	7	US-10-764-818A-12
3	1718.4	39.7	3534	7	US-10-764-818A-13
4	1718.4	39.7	3534	7	US-10-764-818A-14
5	1718.4	39.7	3534	7	US-10-764-818A-15
6	1718.4	39.7	3534	7	US-10-764-818A-29
7	1718.4	39.7	3534	12	US-11-186-282-22
8	1718.4	39.7	4855	7	US-10-764-818A-27
9	1604.2	37.0	5181	12	US-11-094-484-3
10	1604.2	37.0	5181	12	US-11-094-484-3
11	1457.8	33.7	2722	12	US-11-186-282-23
12	1457.8	33.7	2722	12	US-11-186-282-23
13	1456.2	33.6	2700	12	US-11-186-282-33
14	1456.2	33.6	2716	7	US-10-764-818A-19
15	1456.2	33.6	2716	7	US-10-764-818A-20
16	1456.2	33.6	2716	12	US-11-186-282-27
17	1456.2	33.6	2716	12	US-11-186-282-28
18	1456.2	33.6	2716	12	US-11-186-282-29
19	1456.2	33.6	2716	12	US-11-186-282-31
20	1456.2	33.6	2721	12	US-11-186-282-26

21	1456.2	33.6	2721	12	US-11-186-282-34
22	1456.2	33.6	2725	7	US-10-764-818A-30
23	1456.2	33.6	2725	12	US-11-186-282-25
24	1456.2	33.6	2725	12	US-11-186-282-32
25	1456.2	33.6	2739	7	US-10-764-818A-28
26	1456.2	33.6	2739	12	US-11-186-282-30
27	1397.6	32.3	5225	12	US-11-231-725-1
28	1339.2	30.9	6233	12	US-11-193-750-10
29	1294.8	29.9	4432	12	US-11-115-425-12
30	1294.8	29.9	4864	12	US-11-115-425-14
31	1274.4	29.4	2403	7	US-10-523-682-1
32	1197.2	27.6	4886	12	US-11-005-216-4
33	1197.2	27.6	4151	12	US-11-213-368-15
34	1197.2	27.6	4181	12	US-11-170-123-1
35	1197.2	27.6	4183	12	US-11-170-123-2
36	1197.2	27.6	4692	12	US-11-082-154A-29
37	1197.2	27.6	4862	12	US-11-082-154A-87
38	1197.2	27.6	4894	12	US-11-181-148-2
39	1197.2	27.6	7487	12	US-11-181-148-4
40	1195.4	27.6	3913	8	US-10-981-267-27
41	1189.2	27.5	4732	12	US-11-145-532-8
42	1179.8	27.2	4710	12	US-11-131-479-92
43	1179.4	27.2	7765	12	US-11-131-479-110
44	1179.4	27.2	7765	12	US-11-131-479-111
45	1174.6	27.1	2710	7	US-10-764-818A-17

ALIGNMENTS

RESULT 1

US-10-764-818A-11
; Sequence 11, Application US/10764818A
; Publication No. US20040204358A1
; GENERAL INFORMATION:
; APPLICANT: ADVISYS
; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASES CU
; TITLE OF INVENTION: HERD ANIMALS
; FILE REFERENCE: 108328.00170 - AVSI-0033
; CURRENT APPLICATION NUMBER: US/10764,818A
; CURRENT FILING DATE: 2004-01-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 11
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence for the HV-GHRH plasmid.
US-10-764-818A-11

Query Match	39.7%	Score 1718.4	DB 7	Length 3534
Best Local Similarity	90.5%	Pred. No. 7.5e-235		
Matches 1926	Conservative 0	Mismatches 11	Indels 191	Gaps 1
Qy	2205	GCACAGCTCCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTGGCGTAATCAT	2264	
Db	1366	GGCCCGGTACAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTGGCGTAATCAT	1425	
Qy	2265	GGTCATAGCTTTTCTGTGTGAATTTATTCGCTCACAANTTCCACACATACAG	2324	
Db	1426	GGTCATAGCTTTTCTGTGTGAATTTATTCGCTCACAANTTCCACACATACAG	1485	
Qy	2325	CCGGAAGCATAAAGTGTAAAGCTGGGGTGCCTTAATGAGTGAGTCACTACATTAAATG	2384	
Db	1486	CCGGAAGCATAAAGTGTAAAGCTGGGGTGCCTTAATGAGTGAGTCACTACATTAAATG	1545	
Qy	2385	CGTTGGCTCACTGCGCGCTTTCCAGTCGGGAAACCTGTGCGGAGCTGATTAATGAA	2444	
Db	1546	CGTTGGCTCACTGCGCGCTTTCCAGTCGGGAAACCTGTGCGGAGCTGATTAATGAA	1605	
Qy	2445	TCGGCCNACCGCGGGAGGGGTTGGTATTTGGCGCTTTCGCTTCTCGCTCA	2504	

Db 1606 TCGGCCAACCGCGGGGAGAGCGGTTTGCGTATTGGCGCGCTCTTCCGCTTCCTCGCTCA 1665
 Qy 2505 CTGACTCGCTCGCTCGGTCGTTCCGGCTGCGCGAGCGGTATCAGCTCACTCAAGGCGG 2564
 Db 1666 CTGACTCGCTCGCTCGGTCGTTCCGGCTGCGCGAGCGGTATCAGCTCACTCAAGGCGG 1725
 Qy 2565 TAATACGGTTATCCACAGAAATCAGGGGATACGAGGAAAGAAACATGTGAGCAAAAGGCC 2624
 Db 1726 TAATACGGTTATCCACAGAAATCAGGGGATACGAGGAAAGAAACATGTGAGCAAAAGGCC 1785
 Qy 2625 AGCAAAAGGCGAGAAACCGTAAAAAGGCGGTTGCTGGCGGTTTTTTCATAGGCTCGGCC 2684
 Db 1786 AGCAAAAGGCGAGAAACCGTAAAAAGGCGGTTGCTGGCGGTTTTTTCATAGGCTCGGCC 1845
 Qy 2685 CCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGCGAAACCCGACAGGAC 2744
 Db 1846 CCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGCGAAACCCGACAGGAC 1905
 Qy 2745 TATAAGATACAGCGGTTTCCCTCGGAAGCTCCCTCGTCGCTCTCTCTGTTCCGACCC 2804
 Db 1906 TATAAGATACAGCGGTTTCCCTCGGAAGCTCCCTCGTCGCTCTCTCTGTTCCGACCC 1965
 Qy 2805 TCGCGCTTACCGGATACCTGTCGCGCTTTTCCCTTCGGGAAGCGTGGCGCTTTCTCAAT 2864
 Db 1966 TCGCGCTTACCGGATACCTGTCGCGCTTTTCCCTTCGGGAAGCGTGGCGCTTTCTCAT 2025
 Qy 2865 GCTCAGCGTAGGTATCTCAGTTCCGTTGAGTGTGCTTCCGCTCCAAAGCTGGCTGTGTGC 2924
 Db 2026 GCTCAGCGTAGGTATCTCAGTTCCGTTGAGTGTGCTTCCGCTCCAAAGCTGGCTGTGTGC 2085
 Qy 2925 ACGAACCCCGGTTTCAGCGCGACCGCTGCGCTTATCCGTTAACTATCGTCTTGAGTCCA 2984
 Db 2086 ACGAACCCCGGTTTCAGCGCGACCGCTGCGCTTATCCGTTAACTATCGTCTTGAGTCCA 2145
 Qy 2985 ACCCGGTAAGACACGACTTATCGCACCTGGCAGAGCCACTGGTAAACAGGATTAGCAG 3044
 Db 2146 ACCCGGTAAGACACGACTTATCGCACCTGGCAGAGCCACTGGTAAACAGGATTAGCAG 2205
 Qy 3045 CGAGTATGAGCGGTCACAGAGTTCTTGAAGTGTGGCTTAACCTACGGCTACACTA 3104
 Db 2206 CGAGTATGAGCGGTCACAGAGTTCTTGAAGTGTGGCTTAACCTACGGCTACACTA 2265
 Qy 3105 GAAGACAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTG 3164
 Db 2266 GAAGAACAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTG 2325
 Qy 3165 GTAGCTCTTGATCCGGCAAAACAAACCGCTGGTAGCGGTGGTTTTTTTGTTCGAAGC 3224
 Db 2326 GTAGCTCTTGATCCGGCAAAACAAACCGCTGGTAGCGGTGGTTTTTTTGTTCGAAGC 2385
 Qy 3225 AGCAGATTACGGCGCAGAAAAAGGATCTCAAGAAAGATCTTTTGATCTTTTCTACGGGT 3284
 Db 2386 AGCAGATTACGGCGCAGAAAAAGGATCTCAAGAAAGATCTTTTGATCTTTTCTACGGGT 2445
 Qy 3285 CTGACGCTCAGTGGAAACGAAAACTCAGTTAAGGGAATTTGTGTCATGAGCGGATACAT 3344
 Db 2446 CTGACGC----- 2452
 Qy 3345 TTGAATGATTATTAGAAAAATAACAAATAGGGGTTCCGGCGCACATTTCCCGGAAAGTGC 3404
 Db 2453 ----- 2452
 Qy 3405 CACCTGTATCGGTGTAATAACCGCACAGATCGTGAAGGAGAAAAATACCGCATCAGGAA 3464
 Db 2453 ----- 2452
 Qy 3465 ATTGTAAGCGTTAAATTTACAGAACTCGTCAAGAGCGGATAGAGCGGATCGCTG 3524
 Db 2453 -----TCAGAAAGAACTCGTCAAGAGCGGATAGAGCGGATCGCTG 2494
 Qy 3525 CGAATCGGAGCGGCATACCGTAAAGCACGAGGAGCGGTACGCCATTTCGCGCGCAAG 3584
 Db 2495 CGAATCGGAGCGGCATACCGTAAAGCACGAGGAGCGGTACGCCATTTCGCGCGCAAG 2554

Qy 3585 CTCTTCAGCAATATACAGGGTAGCCAAACGCTATGTCTGTATAGCGGTCCGCCACACCCAG 3644
 Db 2555 CTCTTCAGCAATATACAGGGTAGCCAAACGCTATGTCTGTATAGCGGTCCGCCACACCCAG 2614
 Qy 3645 CCGGCCACAGTCGATGATCCAGAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCA 3704
 Db 2615 CCGGCCACAGTCGATGATCCAGAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCA 2674
 Qy 3705 GGCATCCCATGGGTACGACGAGATCCTCGCGTCCGGCATGTCTGCCCTTGAGCCCTGGC 3764
 Db 2675 GGCATCCCATGGGTACGACGAGATCCTCGCGTCCGGCATGTCTGCCCTTGAGCCCTGGC 2734
 Qy 3765 GAACAGTTCGGCTGGCCGAGCCCTGATGCTCTTCGTCAGATCATCTCTGATCGACAAG 3824
 Db 2735 GAACAGTTCGGCTGGCCGAGCCCTGATGCTCTTCGTCAGATCATCTCTGATCGACAAG 2794
 Qy 3825 ACCGGCTTCATCCGAGTACGTCTCGCTCGATCGATGTTTCGCTTGGTGGTCCGAATGG 3884
 Db 2795 ACCGGCTTCATCCGAGTACGTCTCGCTCGATCGATGTTTCGCTTGGTGGTCCGAATGG 2854
 Qy 3885 GCAGGTAGCCGGATCAAGCGGTATGCAGCCCGCATTTGCATCAGCCATGATGGATACCTT 3944
 Db 2855 GCAGGTAGCCGGATCAAGCGGTATGCAGCCCGCATTTGCATCAGCCATGATGGATACCTT 2914
 Qy 3945 CTCGGCAGGACAAAGGTGAGATGACAGAGATCTCTGCCCGGACATTCGCCCAATAGCAG 4004
 Db 2915 CTCGGCAGGACAAAGGTGAGATGACAGAGATCTCTGCCCGGACATTCGCCCAATAGCAG 2974
 Qy 4005 CCAGTCCCTTCCCGCTTCAGTGACAACTCGAGCACAGCTCGCAAGGAACGCCGCTCGT 4064
 Db 2975 CCAGTCCCTTCCCGCTTCAGTGACAACTCGAGCACAGCTCGCAAGGAACGCCGCTCGT 3034
 Qy 4065 GGCCAGCCACATAGCCCGCTGCTCTCTGTCAGTTCATTTCAGGGCACCGGACAGGTC 4124
 Db 3035 GGCCAGCCACATAGCCCGCTGCTCTCTGTCAGTTCATTTCAGGGCACCGGACAGGTC 3094
 Qy 4125 GGTCTTGAAAAAAGAACCGGGCGCCCTGCGCTGACGCCGGAACACGGCGGCATCAGA 4184
 Db 3095 GGTCTTGAAAAAAGAACCGGGCGCCCTGCGCTGACGCCGGAACACGGCGGCATCAGA 3154
 Qy 4185 GCAGCGGATTCCTGTTGTGCCCCAGTCATAGCCGAATAGCTCTCCACCCCAAGCGGCCG 4244
 Db 3155 GCAGCGGATTCCTGTTGTGCCCCAGTCATAGCCGAATAGCTCTCCACCCCAAGCGGCCG 3214
 Qy 4245 AGAACCCTCGTGCAATCCATCTTGTCAATCATGCAAAACGATCTCATCTGTCTCTTG 4304
 Db 3215 AGAACCCTCGTGCAATCCATCTTGTCAATCATGCAAAACGATCTCATCTGTCTCTTG 3274
 Qy 4305 ATCAGAGCTTGATCCCTGCGCCATCAG 4332
 Db 3275 ATCAGATCTTGATCCCTGCGCCATCAG 3302

RESULT 2

US-10-764-818A-12
 ; Sequence 12, Application US/10764818A
 ; Publication No. US20040204358A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ADVISYS
 ; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASES CUI
 ; TITLE OF INVENTION: HERD ANIMALS
 ; FILE REFERENCE: 108328.00170 - AVSI-0033
 ; CURRENT APPLICATION NUMBER: US/10764,818A
 ; CURRENT FILING DATE: 2004-01-26
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 12
 ; LENGTH: 3534
 ; TYPE: DNA
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Sequence for the TI-GHRH plasmid.

US-10-764-818A-12

Query Match 39.7%; Score 1718.4; DB 7; Length 3534;
 Best Local Similarity 90.5%; Pred. No. 7.5e-235;
 Matches 1926; Conservative 0; Mismatches 11; Indels 191; Gaps 1;

Qy	2205	GCACAGCTCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTGGCGTAATCAT	2264
Db	1366	GGCCCGGTACAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTGGCGTAATCAT	1425
Qy	2265	GGTCATAGCTGTTTCCTGCTGTAATTTGTTATCCGCTCAGATTCACACAAATACGAG	2324
Db	1426	GGTCATAGCTGTTTCCTGCTGTAATTTGTTATCCGCTCAGATTCACACAAATACGAG	1485
Qy	2325	CCGGAAGCATAAAGTGTAAAGCTTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTG	2384
Db	1486	CCGGAAGCATAAAGTGTAAAGCTTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTG	1545
Qy	2385	CGTTGCGCTCACTGCGCTTTTCAGTCGGGAAACCTGTGTCGAGCTGCATTAATGAA	2444
Db	1546	CGTTGCGCTCACTGCGCTTTTCAGTCGGGAAACCTGTGTCGAGCTGCATTAATGAA	1605
Qy	2445	TCGSCCAACCGCGGGAGAGGGGTTTGGTATTTGGGCGCTCTTCGCTTCTCGCTCA	2504
Db	1606	TCGSCCAACCGCGGGAGAGGGGTTTGGTATTTGGGCGCTCTTCGCTTCTCGCTCA	1665
Qy	2505	CTGACTCGCTGCGCTCGGCTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAGGCGG	2564
Db	1666	CTGACTCGCTGCGCTCGGCTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAGGCGG	1725
Qy	2565	TAATACGGTTATCCACAGATTCAGGGGATAACCGAGGAAAGAAATGTGAGCAAAAGGCC	2624
Db	1726	TAATACGGTTATCCACAGATTCAGGGGATAACCGAGGAAAGAAATGTGAGCAAAAGGCC	1785
Qy	2625	AGCAAAAGGCCAGGAAACCGTAAAGAGCGCGTGTCTGGCGTTTTCATAGCTCGGC	2684
Db	1786	AGCAAAAGGCCAGGAAACCGTAAAGAGCGCGTGTCTGGCGTTTTCATAGCTCGGC	1845
Qy	2685	CCCTGACGAGCATCAAAAATTCAGCGCTCAAGTTCAGAGGTGGCGAAACCCGACAGGAC	2744
Db	1846	CCCTGACGAGCATCAAAAATTCAGCGCTCAAGTTCAGAGGTGGCGAAACCCGACAGGAC	1905
Qy	2745	TATTAAGATACAGGGCTTTCCCGCTGGAAAGCTCCCTCGTGGCGCTCTCTGTTCCGACCC	2804
Db	1906	TATTAAGATACAGGGCTTTCCCGCTGGAAAGCTCCCTCGTGGCGCTCTCTGTTCCGACCC	1965
Qy	2805	TGCGGCTTACCGGATACCTGCTCGGCTTTCTCCCTTCGGGAAAGCGGTCTTCTCAAT	2864
Db	1966	TGCGGCTTACCGGATACCTGCTCGGCTTTCTCCCTTCGGGAAAGCGGTCTTCTCAAT	2025
Qy	2865	GCTCAGCGTGTAGGTATCTCAGTTTCGGTGTAGGTTCGCTCCAAAGCTGGGCTGTGTC	2924
Db	2026	GCTCAGCGTGTAGGTATCTCAGTTTCGGTGTAGGTTCGCTCCAAAGCTGGGCTGTGTC	2085
Qy	2925	ACGAACCCCGGTTACGCGCGAAGCGTGGCGCTTATCCGGTAACTATCGTCTTTGAGTCCA	2984
Db	2086	ACGAACCCCGGTTACGCGCGAAGCGTGGCGCTTATCCGGTAACTATCGTCTTTGAGTCCA	2145
Qy	2985	ACCGGTTAGACACGACTTATCGCACTGCGACGCGCTATCGGTAAACAGATTTAGCAGAG	3044
Db	2146	ACCGGTTAGACACGACTTATCGCACTGCGACGCGCTATCGGTAAACAGATTTAGCAGAG	2205
Qy	3045	CGAGGTATGTAGCGGCTGTACAGAGTTCTTGAAGTGGTGGCCCTAACTACGGCTACACTA	3104
Db	2206	CGAGGTATGTAGCGGCTGTACAGAGTTCTTGAAGTGGTGGCCCTAACTACGGCTACACTA	2265
Qy	3105	GAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCGAGTTACTCTTCGGAAGAGGTTG	3164
Db	2266	GAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCGAGTTACTCTTCGGAAGAGGTTG	2325
Qy	3165	GTAGCTCTTGATCCGCAACAAACACCGCTGCTAGCGGTGTTTTTTTGTGTTGCAAGC	3224
Db	2326	GTAGCTCTTGATCCGCAACAAACACCGCTGCTAGCGGTGTTTTTTTGTGTTGCAAGC	2385

Qy	3225	AGCAGATTACGCGCAGAAAAAAGGATCTCAAGAGATCCTTTGATCTCTTTCTACGGGT	3284
Db	2386	AGCAGATTACGCGCAGAAAAAAGGATCTCAAGAGATCCTTTGATCTCTTTCTACGGGT	2445
Qy	3285	CTGACGCTCAGTGGAAACGAAACTCACTGTTAAGGGATTTTGGTCATGAGCGGATACATAT	3344
Db	2446	CTGACGCTCAGTGGAAACGAAACTCACTGTTAAGGGATTTTGGTCATGAGCGGATACATAT	3404
Qy	3345	TTGAATGTATTATAGAAAAATAAACAATAGGGGTTTCGGCGCACATTTCCCGGAAAGTGC	3404
Db	2453	TTGAATGTATTATAGAAAAATAAACAATAGGGGTTTCGGCGCACATTTCCCGGAAAGTGC	2452
Qy	3405	CACCTGTATCGGCTGTAATAACCGCACAGATCGCTAAGGAGAAAAATACCGCATCAGGAA	3464
Db	2453	CACCTGTATCGGCTGTAATAACCGCACAGATCGCTAAGGAGAAAAATACCGCATCAGGAA	2452
Qy	3465	ATTGTAAGCTTAAATAATTCAGAAAGAACTCGTCAAGAGCGATAGAAAGCGATGCGCTG	3524
Db	2453	ATTGTAAGCTTAAATAATTCAGAAAGAACTCGTCAAGAGCGATAGAAAGCGATGCGCTG	2494
Qy	3525	CGAATCGGAGCGGCGATACCGTAAAGCAGAGGAAAGCGGTCAAGCCATTTCCGCGCCAAAG	3584
Db	2495	CGAATCGGAGCGGCGATACCGTAAAGCAGAGGAAAGCGGTCAAGCCATTTCCGCGCCAAAG	2554
Qy	3585	CTCTTCAGCAATATACCGGCTAGCCAAACGCTATGCTCTGATAGCGGTCCGCCACACCCAG	3644
Db	2555	CTCTTCAGCAATATACCGGCTAGCCAAACGCTATGCTCTGATAGCGGTCCGCCACACCCAG	2614
Qy	3645	CGGCGCACAGTTCGATGAATCCAGAAAAAGCGGCAATTTTCCACCATGATATTCGGCAAGCA	3704
Db	2615	CGGCGCACAGTTCGATGAATCCAGAAAAAGCGGCAATTTTCCACCATGATATTCGGCAAGCA	2674
Qy	3705	GGCATCGCATGGGTCAAGCAGAGATCCTCGCGCTCGGGCATGCTCGCTTGGAGCTGGC	3764
Db	2675	GGCATCGCATGGGTCAAGCAGAGATCCTCGCGCTCGGGCATGCTCGCTTGGAGCTGGC	2734
Qy	3765	GAACAGTTTCGGCTGGCGCGAGCCCTCGATGCTCTTCGTCCAGATCATCTCTGATCGACAG	3824
Db	2735	GAACAGTTTCGGCTGGCGCGAGCCCTCGATGCTCTTCGTCCAGATCATCTCTGATCGACAG	2794
Qy	3825	ACCGGCTTCATCCAGTACGCTCGCTCGATGCGATGTTTCGCTTGGTGGTTCGATAGG	3884
Db	2795	ACCGGCTTCATCCAGTACGCTCGCTCGATGCGATGTTTCGCTTGGTGGTTCGATAGG	2854
Qy	3885	GCAGGTAGCGGATCAAGCGTATGACCGCGCATTCGATCGATCGATGATGATGATGATGAT	3944
Db	2855	GCAGGTAGCGGATCAAGCGTATGACCGCGCATTCGATCGATCGATGATGATGATGATGAT	2914
Qy	3945	CTCGGAGGAGCAAGGTGAGATGACAGGAGATCCTCGCGCGCATCTTCGCCCAATAGCAG	4004
Db	2915	CTCGGAGGAGCAAGGTGAGATGACAGGAGATCCTCGCGCGCATCTTCGCCCAATAGCAG	2974
Qy	4005	CCAGTCCCTTCCCGCTTTCAGTGAACAGCTCGAGCAGAGCTGGCGAAAGAACGCGCTCGT	4064
Db	2975	CCAGTCCCTTCCCGCTTTCAGTGAACAGCTCGAGCAGAGCTGGCGAAAGAACGCGCTCGT	3034
Qy	4065	GGCGAGCAGATAGCGCGCTCGCTTCGCTTTCGAGTTTCATTCAGGGCACCGGACAGGTC	4124
Db	3035	GGCGAGCAGATAGCGCGCTCGCTTCGCTTTCGAGTTTCATTCAGGGCACCGGACAGGTC	3094
Qy	4125	GGTCTTTCAGAAAAAGAACCGGGCGCCCTCGCTGACAGCGGAAACACCGCGGCATCAGA	4184
Db	3095	GGTCTTTCAGAAAAAGAACCGGGCGCCCTCGCTGACAGCGGAAACACCGCGGCATCAGA	3154
Qy	4185	GCAGCGGATGCTGTTGTCGCGAGTATAGCGGAATAGCTCTTCCACCGAAGCGGCGCG	4244
Db	3155	GCAGCGGATGCTGTTGTCGCGAGTATAGCGGAATAGCTCTTCCACCGAAGCGGCGCG	3214
Qy	4245	AGAACTCGCTGCAATTCATCTTGTTCATCATGCGAAACGATCCTCATCTCTCTCTTG	4304
Db	3215	AGAACTCGCTGCAATTCATCTTGTTCATCATGCGAAACGATCCTCATCTCTCTCTTG	3274

QY 3225 AGCAGATTAGCGCGAGAAAAAGGATCTCAAGAAGATCCTTGATCTTTTACGGGGT 3284
 DB 2386 AGCAGATTACCGCGAGAAAAAGGATCTCAAGAGATCTTTGATCTTTTACGGGGT 2445
 QY 3285 CTGACGCTCAGTGAACGAATACTCAGTTAAGGATTTTGGTCATGAGCGGATACATAT 3344
 DB 2446 CTGACGC----- 2452
 QY 3345 TTGAATGATTTAGAAAAATAAACAAATAGGGTTCCGCGCACATTTCCCGGAAAGTGC 3404
 DB 2453 ----- 2452
 QY 3405 CACCTGATCGGTGTGAATACCGCACAGATCGTAAAGGAGAAAAATACCGCATCAGGAA 3464
 DB 2453 ----- 2452
 QY 3465 ATTGTAAGCGTTAATAATTCAGAGAACTCGTCAAGAGCGGATAGAGCGGATCGCTG 3524
 DB 2453 -----TCAAGAAAGCTCGTCAAGAAAGCGATAGAGCGGATCGCTG 2494
 QY 3525 CGAATCGGAGCGGCGGATACCGTAAAGCACGAGAGCGGTACGCCCATTTCCGCGCAAG 3584
 DB 2495 CGAATCGGAGCGGCGGATACCGTAAAGCACGAGAGCGGTACGCCCATTTCCGCGCAAG 2554
 QY 3585 CTCTTCAGCAATATCACGGGTAGCCAAAGCTATGTCTGTATGAGCGGTCCGCCACACCCAG 3644
 DB 2555 CTCTTCAGCAATATCACGGGTAGCCAAAGCTATGTCTGTATGAGCGGTCCGCCACACCCAG 2614
 QY 3645 CCGGCCACAGTCAGTGAATCCAGAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCA 3704
 DB 2615 CCGGCCACAGTCAGTGAATCCAGAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCA 2674
 QY 3705 GGATCGCCATGGGTACAGACAGATCCTCGCGGTCCGGCATGCTCGCTTTGAGCCTGGC 3764
 DB 2675 GGATCGCCATGGGTACAGACAGATCCTCGCGGTCCGGCATGCTCGCTTTGAGCCTGGC 2734
 QY 3765 GAACAGTTTCGGTGGCGGAGCCCTGATGCTCTTGTCCAGATCATCTGTATGATCGCAAG 3824
 DB 2735 GAACAGTTTCGGTGGCGGAGCCCTGATGCTCTTGTCCAGATCATCTGTATGATCGCAAG 2794
 QY 3825 ACCGGTTCATCCGATAGTCTCGCTCGATCGATGTTTCTGCTTGGTGGTTCGATGG 3884
 DB 2795 ACCGGTTCATCCGATAGTCTCGCTCGATCGATGTTTCTGCTTGGTGGTTCGATGG 2854
 QY 3885 GCAGGTAGCCGGATCAAGCGTATGACAGCCCGCATGTCATGACCATGATGATGATCTTT 3944
 DB 2855 GCAGGTAGCCGGATCAAGCGTATGACAGCCCGCATGTCATGACCATGATGATGATCTTT 2914
 QY 3945 CTCGGCAGGAGCAAGGTGAGATGACAGGAGATCTTCCCGGCACCTTCGCCCAATAGCAG 4004
 DB 2915 CTCGGCAGGAGCAAGGTGAGATGACAGGAGATCTTCCCGGCACCTTCGCCCAATAGCAG 2974
 QY 4005 CCAGTCCCTTCGCTTCAGTGACAGGTTCGAGCAGCTGCGCAAGGACGCCCTCGT 4064
 DB 2975 CCAGTCCCTTCGCTTCAGTGACAGGTTCGAGCAGCTGCGCAAGGACGCCCTCGT 3034
 QY 4065 GGCAGCAGCAGATAGCCGCTCGCTCTTGCAGTTTCAATTCAGGCGCACCGGACAGGTC 4124
 DB 3035 GGCAGCAGCAGATAGCCGCTCGCTCTTGCAGTTTCAATTCAGGCGCACCGGACAGGTC 3094
 QY 4125 GGTCTTGAATAAAGAAACCGGGCGCCCTCGCTGACAGCGGAAACAGCGGCGCATCAGA 4184
 DB 3095 GGTCTTGAATAAAGAAACCGGGCGCCCTCGCTGACAGCGGAAACAGCGGCGCATCAGA 3154
 QY 4185 GCAGCGGATTTCTGTTGTCGCCAGTCATAGCGAATAGCTCTCCACCCCAAGCGGCCG 4244
 DB 3155 GCAGCGGATTTCTGTTGTCGCCAGTCATAGCGAATAGCTCTCCACCCCAAGCGGCCG 3214
 QY 4245 AGAACCTCGGTGCAATCATCTTTGTTCAATCATCGGAAACGATCTCATCTCTCTCTTG 4304
 DB 3215 AGAACCTCGGTGCAATCATCTTTGTTCAATCATCGGAAACGATCTCATCTCTCTCTTG 3274
 QY 4305 ATCAGAGCTTGATCCCTTCGCCCATCAG 4332

DB 3275 ATCAGATCTTGATCCCTCGCCATCAG 3302
 RESULT 6
 US-10-764-818A-29
 ; Sequence 29, Application US/10764818A
 ; Publication No. US20040204358A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ADVISYS
 ; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASES CU
 ; TITLE OF INVENTION: HERD ANIMALS
 ; FILE REFERENCE: 108328.00170 - AVSI-0033
 ; CURRENT APPLICATION NUMBER: US/10/764,818A
 ; CURRENT FILING DATE: 2004-01-26
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 29
 ; LENGTH: 3534
 ; TYPE: DNA
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Codon optimized plasmid for GHRH expression.
 US-10-764-818A-29
 Query Match 39.7%; Score 1718.4; DB 7; Length 3534;
 Best Local Similarity 90.5%; Pred. No. 7.5e-235;
 Matches 1926; Conservative 0; Mismatches 11; Indels 191; Gaps 1;
 QY 2205 GCCACAGCTCCAGCTTTTGTTCCTTTAGTGAGGGTTAATTTTCGAGCTTGGCGTAATCAT 2264
 DB 1366 GGCCCGGTACCAGCTTTTGTTCCTTTAGTGAGGGTTAATTTTCGAGCTTGGCGTAATCAT 1425
 QY 2265 GGTACATAGCTTTTCCTGTGTGAAATTTGTTATCCGCTCACAAATTTCCACAAATACGAG 2324
 DB 1426 GGTACATAGCTTTTCCTGTGTGAAATTTGTTATCCGCTCACAAATTTCCACAAATACGAG 1485
 QY 2325 CCGGAAGCATAAAGTGTAAAGCTCGGGTGCCCTAAATGAGTGAGCTAACTCACATTAATTTG 2384
 DB 1486 CCGGAAGCATAAAGTGTAAAGCTCGGGTGCCCTAAATGAGTGAGCTAACTCACATTAATTTG 1545
 QY 2385 CGTTGCGCTCACTGCGCGCTTTTCAGTCGCGGAAACCTGTCGTCGAGCTGCATTAATGAA 2444
 DB 1546 CGTTGCGCTCACTGCGCGCTTTTCAGTCGCGGAAACCTGTCGTCGAGCTGCATTAATGAA 1605
 QY 2445 TCGGCCAAACGCGCGGAGAGCGGTTTCGCTATTTGGGCGCTTTCGCTTCCGCTCA 2504
 DB 1606 TCGGCCAAACGCGCGGAGAGCGGTTTCGCTATTTGGGCGCTTTCGCTTCCGCTCA 1665
 QY 2505 CTGACTCGCTGCGCTCGGTTCGCTCGGCGAGCGGTATCAGCTCACTCAAAAGCGG 2564
 DB 1666 CTGACTCGCTGCGCTCGGTTCGCTCGGCGAGCGGTATCAGCTCACTCAAAAGCGG 1725
 QY 2565 TAATACGGTTATCCACAGAAATCAGGGGATTAACCGAGAAAGAAACATGTGAGCAAAAGGCC 2624
 DB 1726 TAATACGGTTATCCACAGAAATCAGGGGATTAACCGAGAAAGAAACATGTGAGCAAAAGGCC 1785
 QY 2625 AGCAAAAGCCAGGAAACCGTAAAGCGCGCTTGTGCTGGCTTTTCCATAGGCTCGCC 2684
 DB 1786 AGCAAAAGCCAGGAAACCGTAAAGCGCGCTTGTGCTGGCTTTTCCATAGGCTCGCC 1845
 QY 2685 CCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGAC 2744
 DB 1846 CCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGAC 1905
 QY 2745 TATAAAGATACAGGGGTTTCCCTTGGAAGTCCCTCGTCGCTCTCTCTGTTCCGACCC 2804
 DB 1906 TATAAAGATACAGGGGTTTCCCTTGGAAGTCCCTCGTCGCTCTCTCTGTTCCGACCC 1965
 QY 2805 TCGCGCTTACCGGATACCTGTCGCGCTTTCTCCCTTCGGGAGCGGTGGCGCTTCTCAAT 2864
 DB 1966 TCGCGCTTACCGGATACCTGTCGCGCTTTCTCCCTTCGGGAGCGGTGGCGCTTCTCAAT 2925

RESULT 9

US-10-764-818A-26
; Sequence 26, Application US/10764818A
; Publication No. US20040204358A1
; GENERAL INFORMATION:
; APPLICANT: ADVISYS
; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASES CUL
; TITLE OF INVENTION: HERD ANIMALS
; FILE REFERENCE: 108328.00170 - AVSI-0033
; CURRENT APPLICATION NUMBER: US/10764,818A
; CURRENT FILING DATE: 2004-01-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 3558
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence for the inducible pGR1774 with human GHRH
US-10-764-818A-26

Query Match 39.7%; Score 1718; DB 7; Length 3558;
Best Local Similarity 90.5%; Pred. No. 8.5e-235;
Matches 1925; Conservative 1; Mismatches 11; Indels 191; Gaps 1;

QY	2205	GCCACAGCTCCAGCTTTTGGTCCCTTTAGTCAGGGTTAAATTTTCGAGCTTGGCGTAATCAT	2264
DB	1207	GGCCGGTACCAGCTTTTGGTCCCTTTAGTCAGGGTTAAATTTTCGAGCTTGGCGTAATCAT	1266
QY	2265	GGTCATAGCTGTTTCTGTGTGAATTTGTTAGTCAGGGTTAAATTTTCGAGCTTGGCGTAATCAT	2324
DB	1267	GGTCATAGCTGTTTCTGTGTGAATTTGTTAGTCAGGGTTAAATTTTCGAGCTTGGCGTAATCAT	1326
QY	2325	CCGGAAGCATTAAGTGAAGCTTGGGTGCTTAATGAGTGAGCTAATCATTAATTTG	2384
DB	1327	CCGGAAGCATTAAGTGAAGCTTGGGTGCTTAATGAGTGAGCTAATCATTAATTTG	1386
QY	2385	GGTTGGCTCTACTCCGCTTTTCAGTCGGGAACCTGTGCTGCGCAGCTGCATTAATGA	2444
DB	1387	GGTTGGCTCTACTCCGCTTTTCAGTCGGGAACCTGTGCTGCGCAGCTGCATTAATGA	1446
QY	2445	TCGGCCAAACGCGCGGGAGAGCGGTTTGGTATTGGGCGCTCTTCGCTTCTCGCTCA	2504
DB	1447	TCGGCCAAACGCGCGGGAGAGCGGTTTGGTATTGGGCGCTCTTCGCTTCTCGCTCA	1506
QY	2505	CTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG	2564
DB	1507	CTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG	1566
QY	2565	TAATACGGTTATCCACAGAAATCAGGGGATACGAGAGAAAGCAATGTGAGCAAAAGGCC	2624
DB	1567	TAATACGGTTATCCACAGAAATCAGGGGATACGAGAGAAAGCAATGTGAGCAAAAGGCC	1626
QY	2625	AGCAAAAGGCCAGAAACCGTAAAGGCGCGTTGCTGGCGTTTTCATAGGCTCGGCC	2684
DB	1627	AGCAAAAGGCCAGAAACCGTAAAGGCGCGTTGCTGGCGTTTTCATAGGCTCGGCC	1686
QY	2685	CCCCTGAGGAGCATCACAAATTCAGCTCAAGTCAAGTGCGGAAACCCGACAGGAC	2744
DB	1687	CCCCTGAGGAGCATCACAAATTCAGCTCAAGTCAAGTGCGGAAACCCGACAGGAC	1746
QY	2745	TATAAAGATACAGGCGTTTCCCTCGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCC	2804
DB	1747	TATAAAGATACAGGCGTTTCCCTCGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCC	1806
QY	2805	TGCGCTTACCGGATACCTGTCGCTTTTCTCTTTCGGAAGCGTGCGCTTCTCAAT	2864
DB	1807	TGCGCTTACCGGATACCTGTCGCTTTTCTCTTTCGGAAGCGTGCGCTTCTCTATA	1866
QY	2865	GCTCACGCTGTAGTATCTAGTTTCGGTGTAGGTCGTTTCGCTCAAGCTGGGCTGTGTC	2924

DB	1867	GCTCACGCTGTAGTATCTAGTTTCGGTGTAGGTCGTTTCGCTCAAGCTGGGCTGTGTC	1926
QY	2925	ACGNAACCCCGCTTACGCCCCGACCGCTTTCGGCTTATCGGTAACTATCGTCTTCACTCA	2984
DB	1927	ACGNAACCCCGCTTACGCCCCGACCGCTTTCGGCTTATCGGTAACTATCGTCTTCACTCA	1986
QY	2985	ACCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTAGCAGAG	3044
DB	1987	ACCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTAGCAGAG	2046
QY	3045	CGAGGTATGAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTTAACTACGGCTACACTA	3104
DB	2047	CGAGGTATGAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTTAACTACGGCTACACTA	2106
QY	3105	GAAGCAGATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGAGTTG	3164
DB	2107	GAAGCAGATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGAGTTG	2166
QY	3165	GTAAGTCTTGTATCCGCAAAACAAACCCGCTGGTAGCGGTGGTTTTTTTGTTCGCAAGC	3224
DB	2167	GTAAGTCTTGTATCCGCAAAACAAACCCGCTGGTAGCGGTGGTTTTTTTGTTCGCAAGC	2226
QY	3225	AGCAGATTACGCGCAGAAAAAAGGATCTCAAGAGATCTTTCGATCTTTCTACGGGGT	3284
DB	2227	AGCAGATTACGCGCAGAAAAAAGGATCTCAAGAGATCTTTCGATCTTTCTACGGGGT	2286
QY	3285	CTGACGCTCAGTGGAAACGAAAACTCAGCTTAAAGGATTTTGGTCTATGAGCGGATACAT	3344
DB	2287	CTGACGCTCAGTGGAAACGAAAACTCAGCTTAAAGGATTTTGGTCTATGAGCGGATACAT	2293
QY	3345	TTGAATGATTTTAGAAAAATAAATAAGGGTTTCGCGCAGCATTTTCCCGAAAGATGC	3404
DB	2294	TTGAATGATTTTAGAAAAATAAATAAGGGTTTCGCGCAGCATTTTCCCGAAAGATGC	2293
QY	3405	CACCTGTATCGGTGTGAAATATACCGCACAGATCGGTAAAGAGAAAAATACCGCATCAGAA	3464
DB	2294	CACCTGTATCGGTGTGAAATATACCGCACAGATCGGTAAAGAGAAAAATACCGCATCAGAA	2293
QY	3465	ATTGTAAGCGTTAATTAATTCAGAAAGAACTCGTCAAGAGGCGATAGAGGCGATGCGGTG	3524
DB	2294	ATTGTAAGCGTTAATTAATTCAGAAAGAACTCGTCAAGAGGCGATAGAGGCGATGCGGTG	2294
QY	3525	CGAATCGGGAGCGGCGATACCGTAAAGACAGAGAGAAAGCGGTTCAGCCCATTTCCGCGCAAG	3584
DB	2336	CGAATCGGGAGCGGCGATACCGTAAAGACAGAGAGAAAGCGGTTCAGCCCATTTCCGCGCAAG	2395
QY	3585	CTCTTCAGCAATATCAGCGGTAGCAACGCTATGCTCTGATAGCGGTTCGCGCACACCCAG	3644
DB	2396	CTCTTCAGCAATATCAGCGGTAGCAACGCTATGCTCTGATAGCGGTTCGCGCACACCCAG	2455
QY	3645	CCGCGCACAGTCCGATGAATCCAGAAAGCGGCCATTTTCCACCATGATATTTCCGCAAGCA	3704
DB	2456	CCGCGCACAGTCCGATGAATCCAGAAAGCGGCCATTTTCCACCATGATATTTCCGCAAGCA	2515
QY	3705	GGCATCGCCATGGGTCAACGAGAGATCTCTCGCGTGGGCGATGCTCGCTTGAAGCTGGC	3764
DB	2516	GGCATCGCCATGGGTCAACGAGAGATCTCTCGCGTGGGCGATGCTCGCTTGAAGCTGGC	2575
QY	3765	GAACAGTTTCGGCTGGCGCGAGCCCTGATGCTCTTCGTCAGATCATCTGATGTCAGCAAG	3824
DB	2576	GAACAGTTTCGGCTGGCGCGAGCCCTGATGCTCTTCGTCAGATCATCTGATGTCAGCAAG	2635
QY	3825	ACCGGCTTCCATCCGAGTACGCTCGCTCGATGCGATGTTTTCGCTGGTGGTCCGATGG	3884
DB	2636	ACCGGCTTCCATCCGAGTACGCTCGCTCGATGCGATGTTTTCGCTGGTGGTCCGATGG	2695
QY	3885	GCAGGTAGCGGATCAAGCGTATGACAGCCCGCGCATTTGATCATGAGCCATGATGATCTTT	3944
DB	2696	GCAGGTAGCGGATCAAGCGTATGACAGCCCGCGCATTTGATCATGAGCCATGATGATCTTT	2755
QY	3945	CTCGGAGGAGCAAGGTGAGATCAAGGAGATCTTCGCGCGGCACTTCGCGCCATAGCAG	4004
DB	2756	CTCGGAGGAGCAAGGTGAGATCAAGGAGATCTTCGCGCGGCACTTCGCGCCATAGCAG	2815


```
QY 3824 GACCGGCTTCATCCGAGTACGTGCTCGCTCGATCGCATGTTTCGCTTGGTGGTCAATG 3883
DB 3862 GACCGGCTTCATCCGAGTACGTGCTCGCTCGATCGCATGTTTCGCTTGGTGGTCAATG 3803
QY 3884 GCGAGGTAGCGGATCAAGCGTATGACGCGCGCGCATTTGCAATCAGCCATGATGATCTT 3943
DB 3802 GCGAGGTAGCGGATCAAGCGTATGACGCGCGCGCATTTGCAATCAGCCATGATGATCTT 3743
QY 3944 TCTCGGAGGAGCAAGGTGAGATGACAGGAGATCTGCGCGCGCATTTGCGCCCAATAGCA 4003
DB 3742 TCTCGGAGGAGCAAGGTGAGATGACAGGAGATCTGCGCGCGCATTTGCGCCCAATAGCA 3683
QY 4004 GCGAGTCCCTTCGCGCTTCAGTGACAAAGTGCAGACAGTGCAGAAAGCGCCGCTCG 4063
DB 3682 GCGAGTCCCTTCGCGCTTCAGTGACAAAGTGCAGACAGTGCAGAAAGCGCCGCTCG 3623
QY 4064 TGGCCAGCCAGATAGCGCGCTCGCTCGCTTCGCTTCGCTTCATTCAGGGCAGCGACAGGT 4123
DB 3622 TGGCCAGCCAGATAGCGCGCTCGCTCGCTTCGCTTCGCTTCATTCAGGGCAGCGACAGGT 3563
QY 4124 CGGTCTTGACAAAAGAACCGGGCGCCCTCGCTTGACAGCGCGAAACACGGCGGCATCAG 4183
DB 3562 CGGTCTTGACAAAAGAACCGGGCGCCCTCGCTTGACAGCGCGAAACACGGCGGCATCAG 3503
QY 4184 AGCAGCCGATGTCTGTGTTGCCAGTCAATAGCCGAATAGCTCTCCACCCCAAGCGCGC 4243
DB 3502 AGCAGCCGATGTCTGTGTTGCCAGTCAATAGCCGAATAGCTCTCCACCCCAAGCGCGC 3443
QY 4244 GAGAACCTGCGTGAATCAATCTGTTCAATCATGCGAAGATCTCTCTCTCTCTT 4303
DB 3442 GAGAACCTGCGTGAATCAATCTGTTCAATCATGCGAAGATCTCTCTCTCTCTT 3383
QY 4304 GATCAGAGCTTGATCCCTCGGCCATCAG 4332
DB 3382 GATCAGAGCTTGATCCCTCGGCCATCAG 3354

RESULT 11
US-11-186-282-23
; Sequence 23, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
; APPLICANT: Advlsys, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328.000265 AVSI-0042
; CURRENT APPLICATION NUMBER: US/11/186,282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 2722
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Plasmid vector having a codon optimized mouse GHRH sequence
US-11-186-282-23

Query Match 33.7%; Score 1457.8; DB 12; Length 2722;
Best Local Similarity 88.9%; Pred. No. 5.9e-198;
Matches 1664; Conservative 0; Mismatches 27; Indels 180; Gaps 1;

QY 2462 AGAGCGGTTGGCGTATTGGCGGCTCTTCGCTTCCTCGCTCACTGACTCGCTCGCTCG 2521
DB 860 AGTGAGGGTTAAATTCGAGCTTGGTCTTCGCTTCCTCGCTCACTGACTCGCTCGCTCG 919
QY 2522 GTCCGTCGCGCGGAGCGGTATCAGCTCACTCAAGGCGGTAAATCGGTTATCCACA 2581
DB 920 GTCCGTCGCGCGGAGCGGTATCAGCTCACTCAAGGCGGTAAATCGGTTATCCACA 979
QY 2582 GAATCAGGGATATACGAGGAAAGAAACATGTGAGCAAAAGCCAGCAAAAGCGCAGGAAC 2641
DB 980 GAATCAGGGATATACGAGGAAAGAAACATGTGAGCAAAAGCCAGCAAAAGCGCAGGAAC 1039
```

```
QY 2642 CGTAAAGAGCGCGTGTGCTGGCGTCTTTTCCATAGGCTCCGCCCCCTCCAGAGCATCAC 2701
DB 1040 CGTAAAGAGCGCGTGTGCTGGCGTCTTTTCCATAGGCTCCGCCCCCTCCAGAGCATCAC 1099
QY 2702 AAAAATCGAGCGCTCAAGTCAAGGTGCGGAAACCCGACAGGACTATATAAGATACAGGCG 2761
DB 1100 AAAAATCGAGCGCTCAAGTCAAGGTGCGGAAACCCGACAGGACTATATAAGATACAGGCG 1159
QY 2762 TTTCCCGCTGGAAGCTCCCTCGTGGCTCTCTCTGCTCCGACCCCTGCGCTTACCGGATAC 2821
DB 1160 TTTCCCGCTGGAAGCTCCCTCGTGGCTCTCTCTGCTCCGACCCCTGCGCTTACCGGATAC 1219
QY 2822 CTGTCGCGCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCAATGCTCACGCTGATAGTAT 2881
DB 1220 CTGTCGCGCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCAAGCTGATAGTAT 1279
QY 2882 CTGATTCGGTGTAGTGGTTCGCTCAAGTGGGCTGTGTGACGAACCCCGCTTCAG 2941
DB 1280 CTGATTCGGTGTAGTGGTTCGCTCAAGTGGGCTGTGTGACGAACCCCGCTTCAG 1339
QY 2942 CCCGACCGCTGCGCTTTATCCGGTAACTATGCTCTGAGTCCAAACCCGCTAAGACACGAC 3001
DB 1340 CCCGACCGCTGCGCTTTATCCGGTAACTATGCTCTGAGTCCAAACCCGCTAAGACACGAC 1399
QY 3002 TTATCGCCACTGGCAGCAGCCACTGTGTAAACAGGATTAGCAGAGCGAGGTATGTAGCGGT 3061
DB 1400 TTATCGCCACTGGCAGCAGCCACTGTGTAAACAGGATTAGCAGAGCGAGGTATGTAGCGGT 1459
QY 3062 GCTACAGAGTTCTTGAAGTGGTGGCTTAACTAATCGGCTACACTAGAAAGCAAGTATTTGGT 3121
DB 1460 GCTACAGAGTTCTTGAAGTGGTGGCTTAACTAATCGGCTACACTAGAAAGCAAGTATTTGGT 1519
QY 3122 ATCTGCGCTCTGCTGAAGCCAGTTTACCTTCGGAAGGAGTTGCTAGCTCTTTGATTCGGC 3181
DB 1520 ATCTGCGCTCTGCTGAAGCCAGTTTACCTTCGGAAGGAGTTGCTAGCTCTTTGATTCGGC 1579
QY 3182 AAAACAAACACCGCTGGTAGCGGTGTTTTTTTGTTCGAAAGCAGCAGATTTACGCGCAGA 3241
DB 1580 AAAACAAACACCGCTGGTAGCGGTGTTTTTTTGTTCGAAAGCAGCAGATTTACGCGCAGA 1639
QY 3242 AAAAAGGATCTCAAGAGATCTTTTGAATCTTTTCTAGCGGGTCTGAGCTCAGTGGNAC 3301
DB 1640 AAAAAGGATCTCAAGAGATCTTTTGAATCTTTTCTAGCGGGTCTGAGCTCAGTGGNAC 1693
QY 3302 GAAAACTACGTTAAGGGATTTTGGTTCATGAGCGGATACATATTTGAATGTATTAGAAA 3361
DB 1694 ----- 1693
QY 3362 AATAAAACAAATAGGGGTTCGCGCACATTTTCCCGGAAAGTGCACCTGTATGCGGTGTG 3421
DB 1694 ----- 1693
QY 3422 AAATACCGCACAGATGCGTAAGGAGAAATAACCGCATCAGAAATTTGTAAGCGTTAATAA 3481
DB 1694 -----CTAGCG 1699
QY 3482 TTCAGAAGAACTCGTCAAGAAAGCGATAGAAAGGCGATGCGTGGAAATCGGAGCGCGCA 3541
DB 1700 CTCAGAAGAACTCGTCAAGAAAGCGATAGAAAGGCGATGCGTGGAAATCGGAGCGCGCA 1759
QY 3542 TACCGTAAAGCAAGGAGCGGTTCAGCCCAATTCGCGCGCAAGCTCTTCAGCAATATCAC 3601
DB 1760 TACCGTAAAGCAAGGAGCGGTTCAGCCCAATTCGCGCGCAAGCTCTTCAGCAATATCAC 1819
QY 3602 GGGTAGCCAAAGCTATGCTCTGATAGGGTCCGCGCACCCAGCGCGCCACAGTCGATGA 3661
DB 1820 GGGTAGCCAAAGCTATGCTCTGATAGGGTCCGCGCACCCAGCGCGCCACAGTCGATGA 1879
QY 3662 ATCCAGAAAAGCGCGCATTTTCCACCATGATATTCGGAAGAGCGGATCGCCATGGGTCA 3721
DB 1880 ATCCAGAAAAGCGCGCATTTTCCACCATGATATTCGGAAGAGCGGATCGCCATGGGTCA 1939
QY 3722 CGAGAGATCTCTCGCGTCGCGGCAATGCTCGCCTTGAGCCTTGGCGAAACAGTTTCGCTGGCG 3781
```


Db	1940	CGACGAGATCCTCGCCGTCGGGATCGCGCCTTGAGCTGGCGAACAGTTCCGCTGGCG	1999
Qy	3782	CGAGCCCTCATGCTCTTTCGTCCAGATCATCTCGATCGACAAGACCGGCTTCATCCGAG	3841
Db	2000	CGAGCCCTCATGCTCTTTCGTCCAGATCATCTCGATCGACAAGACCGGCTTCATCCGAG	2059
Qy	3842	TACGTGTCGTCGATGCGATGTTTTCCGTTGGTGGTCGAATGGGCAAGGTAGCCGATCAA	3901
Db	2060	TACGTGTCGTCGATGCGATGTTTTCCGTTGGTGGTCGAATGGGCAAGGTAGCCGATCAA	2119
Qy	3902	GCGTATCAGCCGCGCATTCAGTCAGCCATGATGGATACTTTCTCGCAGGAGCAAGGT	3961
Db	2120	GCGTATCAGCCGCGCATTCAGTCAGCCATGATGGATACTTTCTCGCAGGAGCAAGGT	2179
Qy	3962	GAGATGACGAGAGATCTGCCCCGGGCATTTGGCCCAATAGCAGCCAGTCCCTCCCGCTT	4021
Db	2180	GAGATGACGAGAGATCTGCCCCGGGCATTTGGCCCAATAGCAGCCAGTCCCTCCCGCTT	2239
Qy	4022	CAGTGACAAAGTTCGAGCACAGCTCGGCAGAGAAACGCCCGTCGTGGCCAGCCAGTAGCC	4081
Db	2240	CAGTGACAAAGTTCGAGCACAGCTCGGCAGAGAAACGCCCGTCGTGGCCAGCCAGTAGCC	2299
Qy	4082	GCGCTGCTCGTCTTTGAGTTCAATTCAGGGCAACCGACAGGTCGGTCTTGACAAAAGAA	4141
Db	2300	GCGCTGCTCGTCTCGTAGTTCAATTCAGGGCAACCGACAGGTCGGTCTTGACAAAAGAA	2359
Qy	4142	CCGGGCGCCCTGGCTGTACAGCCGGAAACACGGCGGCATCAGAGCAGCCGATTTGTCTGTT	4201
Db	2360	CCGGGCGCCCTGGCTGTACAGCCGGAAACACGGCGGCATCAGAGCAGCCGATTTGTCTGTT	2419
Qy	4202	GTGCCCGATCATAGCCGAATAGCTCTCCACCCAAAGCGGCGGAGAACCTCGGTGCATC	4261
Db	2420	GTGCCCGATCATAGCCGAATAGCTCTCCACCCAAAGCGGCGGAGAACCTCGGTGCATC	2479
Qy	4262	CATCTTGTTCAATCATCGAAAACGATCCTCATCTGTCTCTTGATCAGAGCTTGATCCCC	4321
Db	2480	CATCTTGTTCAATCATCGAAAACGATCCTCATCTGTCTCTTGATCAGATCTTGATCCCC	2539
Qy	4322	TGCGCCATCAG	4332
Db	2540	TGCGCCATCAG	2550

```

RESULT 12
; US-11-186-282-24
; Sequence 24, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
; APPLICANT: Advisys, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328.000265 AVSI-0042
; CURRENT APPLICATION NUMBER: US/11/186,282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 2725
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Plasmid vector having a codon optimized rat GHRH sequence
; US-11-186-282-24

```

	Query Match	33.7%;	Score 1457.8;	DB 12;	Length 2725;
	Best Local Similarity	88.9%;	Pred. No. 5.9e-198;		
	Matches 1664;	Conservative 0;	Mismatches 27;	Indels 180;	Gaps 1;
QY	2462	AGAGCGGCTTTGCGTATTGGCGCTCTTCCGCTTCTCGCTCACTGACTCGCTCGGCTCG	2521		
Db	863	AGTGAGGGTTAAATTTTCGAGCTTGGTCTTCGCTTCTCGCTCACTGACTCGCTCGGCTCG	922		
OV	2532	GTTCGTTCCGCTTCGCGGAGCGGTATCAGCTCACTCAAAAGGCGGTAAATACGGTTATCCACA	2581		

Db	923		GTCTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAGCGGTAATACGGTTATCCACA	982
Qy	2582	GAATCAGGGGATTAACGACGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC	2641	
Db	983	GAATCAGGGGATTAACGACGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC	1042	
Qy	2642	CGTAAAGGCCGCGTGTCTGGGCTTTTCATAGAGCTCGGCCCCCTCAGCAGGATCAC	2701	
Db	1043	CGTAAAGGCCGCGTGTCTGGGCTTTTCATAGAGCTCGGCCCCCTCAGCAGGATCAC	1102	
Qy	2702	AAAAATCGACGCTCAAGTCAAGGTGGCGAAACCCGACAGGACTATAAAGATACACAGGCG	2761	
Db	1103	AAAAATCGACGCTCAAGTCAAGGTGGCGAAACCCGACAGGACTATAAAGATACACAGGCG	1162	
Qy	2762	TTTCCCGCTGGAAAGCTCCCTCGTGGGCTCTCTGTTCGACCCCTGCGCTTACCGGATPAC	2821	
Db	1163	TTTCCCGCTGGAAAGCTCCCTCGTGGGCTCTCTGTTCGACCCCTGCGCTTACCGGATPAC	1222	
Qy	2822	CTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCAATGCTCAGCTCTAGGTAT	2881	
Db	1223	CTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCAATGCTCAGCTCTAGGTAT	1282	
Qy	2882	CTCAGTTCGGTGTAGTTCGCTCCAAAGCTGGGCTGTGTGACGAAACCCCGCTTCAG	2941	
Db	1283	CTCAGTTCGGTGTAGTTCGCTCCAAAGCTGGGCTGTGTGACGAAACCCCGCTTCAG	1342	
Qy	2942	CCGACCGCTGCGCTTATCCCGGTAACTATCGTCTTGAGTCCAAACCGGTAAACACGAC	3001	
Db	1343	CCGACCGCTGCGCTTATCCCGGTAACTATCGTCTTGAGTCCAAACCGGTAAACACGAC	1402	
Qy	3002	TTATCGGCACCTGGCAGCAGCCACTGGGTAAACAGGATTAGCAGAGCGAGGTATGAGCGGT	3061	
Db	1403	TTATCGGCACCTGGCAGCAGCCACTGGGTAAACAGGATTAGCAGAGCGAGGTATGAGCGGT	1462	
Qy	3062	GCTACAGAGTTCTTGAAGTGGTGCCCTAACTACGGCTACACTAGAAGGACAGTATTTGGT	3121	
Db	1463	GCTACAGAGTTCTTGAAGTGGTGCCCTAACTACGGCTACACTAGAAGGACAGTATTTGGT	1522	
Qy	3122	ATCTCGGCTCTGTGAAGCAGTTACCTTCGGAAAGAGTGTGTAGCTCTTCATCCGGC	3181	
Db	1523	ATCTCGGCTCTGTGAAGCAGTTACCTTCGGAAAGAGTGTGTAGCTCTTCATCCGGC	1582	
Qy	3182	AAACAAACCCCGCTGTGTAGCGGTGTTTTTTTGTTCGAAGCAGCAGATTAACGCGAGA	3241	
Db	1583	AAACAAACCCCGCTGTGTAGCGGTGTTTTTTTGTTCGAAGCAGCAGATTAACGCGAGA	1642	
Qy	3242	AAAAAGGATCTCAAGAGATCTTTTCATCTTTTCTACGGGTCTGACGCTCAGTGGAAAC	3301	
Db	1643	AAAAAGGATCTCAAGAGATCTTTTCATCTTTTCTACGGGTCTGACGCTCAGTGGAAAC	1696	
Qy	3302	GAAGAACTCACGTTAAGGGATTTTGGTTCATGACGGGATACATATTGTAATGTATTTAGAAA	3361	
Db	1697	-----	1696	
Qy	3362	AATAAACAAATAGGGTTCCGGGCACATTTCCCGAAAGATGCCACCTGTATCGGGTGTG	3421	
Db	1697	-----	1696	
Qy	3422	AAATACGCACAGATGCGTAAGGAGAAAAATACCGCATCAGGAAATTGTGAAGCGTTAATAA	3481	
Db	1697	-----	1702	
Qy	3482	TTCAGAGAACTCGTCAAGAAAGGCGATAGAAGCGATCGCTGCGAATCCGAGCGGCGA	3541	
Db	1703	CTCAGAAAGAACTCGTCAAGAAAGGCGATAGAAGCGGATCGCTGCGAATCCGAGCGGCGA	1762	
Qy	3542	TACCGTAAAGCAGCAGGAAAGCGGTACGCCATTCGCGCCCAAGCTCTTCAGCAATATCAC	3601	
Db	1763	TACCGTAAAGCAGCAGGAAAGCGGTACGCCATTCGCGCCCAAGCTCTTCAGCAATATCAC	1822	
Qy	3602	GGGTAGCCAAACGCTATGCTGTATAGCGGTCCGCCACACCCAGCGCGCCAGTCTGATGA	3661	

```

Db      1823 GGGTAGCCAGCTATGTCCTGATAGCGGTCCGCCACACCCGCCGCCACAGTGA 1882
Qy      3662 ATCCGAAAAGCGGCCATTTCCTACCATGATATTTGGCAGAGGCAATCGCCATG 3721
Db      1883 ATCCGAAAAGCGGCCATTTCCTACCATGATATTTGGCAGAGGCAATCGCCATG 1942
Qy      3722 CGACGAGATTCCTCGCGGCGATGCTGCTTGAAGCTGGGAAAGTTGCGGTGGC 3781
Db      1943 CGACGAGATTCCTCGCGGCGATGCTGCTTGAAGCTGGGAAAGTTGCGGTGGC 2002
Qy      3782 CGAGCCCTGATGCTCTTCTGTCAGATCATCTGATGCAAGACCGGCTTCATCCG 3841
Db      2003 CGAGCCCTGATGCTCTTCTGTCAGATCATCTGATGCAAGACCGGCTTCATCCG 2062
Qy      3842 TACGTCCTGCTCGATGCGATGTTTTCGCTTGGTGGTCAATGGGCAAGTAC 3901
Db      2063 TACGTCCTGCTCGATGCGATGTTTTCGCTTGGTGGTCAATGGGCAAGTAC 2122
Qy      3902 GCGTATGAGCGCGCGCATGTCATGAGCATGATGATGATCTTTCGCGAGGAGAG 3961
Db      2123 GCGTATGAGCGCGCGCATGTCATGAGCATGATGATGATCTTTCGCGAGGAGAG 2182
Qy      3962 GAGATGACAGAGATCTGCGCCCGGCACTTCGCCAATAGCAGCATCCCTCCGCT 4021
Db      2183 GAGATGACAGAGATCTGCGCCCGGCACTTCGCCAATAGCAGCATCCCTCCGCT 2242
Qy      4022 CAGTGACACAGTCCAGCAACAGTGGCGAGAGAACCCCGTGGCCAGCCAGTAG 4081
Db      2243 CAGTGACACAGTCCAGCAACAGTGGCGAGAGAACCCCGTGGCCAGCCAGTAG 2302
Qy      4082 GCGCTGCTGCTGCTGAGTTGATTCAGGGGACCGGAGAGGTCGCTTGA 4141
Db      2303 GCGCTGCTGCTGCTGAGTTGATTCAGGGGACCGGAGAGGTCGCTTGA 2362
Qy      4142 CCGGCGCGCCCTGCGCTGACAGCCGGAACACCGCGGCAATCAGAGAGCGCAT 4201
Db      2363 CCGGCGCGCCCTGCGCTGACAGCCGGAACACCGCGGCAATCAGAGAGCGCAT 2422
Qy      4202 GTGCCCAATCATAGCCGAATAGCTCTTCAACCAAGCGGCGGAGAACCTGCT 4261
Db      2423 GTGCCCAATCATAGCCGAATAGCTCTTCAACCAAGCGGCGGAGAACCTGCT 2482
Qy      4262 CATCTGTTCAATCATAGCGAAACGATCTCATCTGCTTGTAGCAGAGCTGAT 4321
Db      2483 CATCTGTTCAATCATAGCGAAACGATCTCATCTGCTTGTAGCAGATCTGAT 2542
Qy      4322 TGCGCCATCAG 4332
Db      2543 TGCGCCATCAG 2553

RESULT 13
US-11-186-282-33
; Sequence 33, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
; APPLICANT: AdviaSys, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328.000265 AVSI-0042
; CURRENT APPLICATION NUMBER: US/11/186,282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33
; LENGTH: 2700
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: This is the optimized plasmid for Horse GHRH.
US-11-186-282-33
Query Match      33.6%; Score 1456.2; DB 12; Length 2700;
Best Local Similarity 88.9%; Pred. No. 9.9e-198;

```

```

Matches 1663; Conservative 0; Mismatches 28; Indels 180; Gaps 1;
Qy      2462 AGAGCGGTTTGCCTATTGGGCGCTTTCGCTTCTCTGCTACTGACTGCTGCTG 2521
Db      859 AGTAGGGTTAATTTCAGACTTGGCTTCCCTTCCTGCTCACTGACTGCTGCTGCTG 918
Qy      2522 GTGCTTGGGCTGCGCGCGGCGGCTGATACGCTCACTCAAGGGGGTAAATACGCTT 2581
Db      919 GTGCTTGGGCTGCGCGCGGCGGCTGATACGCTCACTCAAGGGGGTAAATACGCTT 978
Qy      2582 GAATCAGGGGTAACGACGAGAAACATGTGACCAAAAGGCCAGCAAAAGCCAGAAC 2641
Db      979 GAATCAGGGGTAACGACGAGAAACATGTGACCAAAAGGCCAGCAAAAGCCAGAAC 1038
Qy      2642 GGTAAAAAGCGCGGTTGCTGCGCTTTTTCATAGGCTCCGCCCTGACGAGCATAC 2701
Db      1039 GGTAAAAAGCGCGGTTGCTGCGCTTTTTCATAGGCTCCGCCCTGACGAGCATAC 1098
Qy      2702 AAAAATGACGCTCAAGTCAAGAGTGGCGGAAACCGACAGGACTTAATAAGATCA 2761
Db      1099 AAAAATGACGCTCAAGTCAAGAGTGGCGGAAACCGACAGGACTTAATAAGATCA 1158
Qy      2762 TTTCCCGCTGGAAGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2821
Db      1159 TTTCCCGCTGGAAGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1218
Qy      2822 CTGTCGCGCTTTCCTCTTGGGAAACGCTGGCGCTTTCATAGCTCAAGCTGATAT 2881
Db      1219 CTGTCGCGCTTTCCTCTTGGGAAACGCTGGCGCTTTCATAGCTCAAGCTGATAT 1278
Qy      2882 CTCAGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2941
Db      1279 CTCAGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1338
Qy      2942 CCGGACGCTGCTGCTTATCCGCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3001
Db      1339 CCGGACGCTGCTGCTTATCCGCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1398
Qy      3002 TTATGCGCATGCGACGACCATGCTGTAACAGATTAAGACGAGGATATGAGCGCT 3061
Db      1399 TTATGCGCATGCGACGACCATGCTGTAACAGATTAAGACGAGGATATGAGCGCT 1458
Qy      3062 GCTACAGAGTCTTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3121
Db      1459 GCTACAGAGTCTTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1518
Qy      3122 ATCTGCGCTGCTGTAAGCAGTACCTTCGGAAGAAAGTGTGTAAGCTTGTATCC 3181
Db      1519 ATCTGCGCTGCTGTAAGCAGTACCTTCGGAAGAAAGTGTGTAAGCTTGTATCC 1578
Qy      3182 AAACAAACACCGCTGCTGTAAGCAGTACCTTCGGAAGAAAGTGTGTAAGCTTGT 3241
Db      1579 AAACAAACACCGCTGCTGTAAGCAGTACCTTCGGAAGAAAGTGTGTAAGCTTGT 1638
Qy      3242 AAAAAGGATCTCAAGAAATCTTGAATCTTCTACGGGCTGACGCTGAGTGAAC 3301
Db      1639 AAAAAGGATCTCAAGAAATCTTGAATCTTCTACGGGCTGAGGCTGAG----- 1692
Qy      3302 GAAAACCTCAGTTAAGGATTTTGTGATGAGCGGATACATATTTGATTTAGAAA 3361
Db      1693 ----- 1692
Qy      3362 AATAAACAATAGGGGTTCCGCGCACTTCCCGAAAAGTGCACCTGTATGCGGTGT 3421
Db      1693 ----- 1692
Qy      3422 AATATCGCACAGATGCGTAAGAGAAATATCCGATCAGGAATTTGTAACGTTAATA 3481
Db      1693 -----CTAGCG 1698
Qy      3482 TTCAAGAAACTGCTCAAGAGGAGATGAGAGGAGTGCCTGCGAATCCGAGCGGCG 3541
Db      1699 CTCAGAGAACTGCTCAAGAGGAGATGAGAGGAGTGCCTGCGAATCCGAGCGGCG 1758

```

```

QY 3542 TACCGTAAAGCAGGAGGAGCGGTGAGCCCATTCGCCGCCAAGCTTTCAGCAATATAC 3601
    |||
Db 1759 TACCGTAAAGCAGGAGGAGCGGTGAGCCCATTCGCCGCCAAGCTTTCAGCAATATAC 1818
QY 3602 GGGTAAAGCAGGATGCTGCTGATAGCGGTGCGGACACCCAGCGGACAGTGCATGA 3661
    |||
Db 1819 GGGTAAAGCAGGATGCTGCTGATAGCGGTGCGGACACCCAGCGGACAGTGCATGA 1878
QY 3662 ATCCAGAAAGCGGCAATTTTTCACCATGATATTCGGCAAGGAGCATGCGCATGCTCA 3721
    |||
Db 1879 ATCCAGAAAGCGGCAATTTTTCACCATGATATTCGGCAAGGAGCATGCGCATGCTCA 1938
QY 3722 CGACGAGATCTTCGCGGTGCGGACAGTCTGCTTGAAGCTTGGCGAAAGTTGCGTGGCG 3781
    |||
Db 1939 CGACGAGATCTTCGCGGTGCGGACAGTCTGCTTGAAGCTTGGCGAAAGTTGCGTGGCG 1998
QY 3782 CGAGCCCGTGAATGCTTCTGTCAGATCATCTCTGATCGACAAGACCGGCTTCATCCAG 3841
    |||
Db 1999 CGAGCCCGTGAATGCTTCTGTCAGATCATCTCTGATCGACAAGACCGGCTTCATCCAG 2058
QY 3842 TACGCTCTGCTCGATGCGATGTTTCGCTTGGTGGTGAATGGAGAGGTAGCCGATCAA 3901
    |||
Db 2059 TACGCTCTGCTCGATGCGATGTTTCGCTTGGTGGTGAATGGAGAGGTAGCCGATCAA 2118
QY 3902 GCGTATGACGCGCGCGCATTCATCAGCCATGATGATATCTTCTTCGCGAGAGCAAGGT 3961
    |||
Db 2119 GCGTATGACGCGCGCGCATTCATCAGCCATGATGATATCTTCTTCGCGAGAGCAAGGT 2178
QY 3962 GAGATGACAGAGATCTGCGCCCGGCACTTCGCCCAATAGCAGCAGTCCCTCCGCTT 4021
    |||
Db 2179 GAGATGACAGAGATCTGCGCCCGGCACTTCGCCCAATAGCAGCAGTCCCTCCGCTT 2238
QY 4022 CAGTGAACAAGTGAAGCAGCTGCGCAAGAAACGCCGTGCTGTCAGCCACGATAGCC 4081
    |||
Db 2239 CAGTGAACAAGTGAAGCAGCTGCGCAAGAAACGCCGTGCTGTCAGCCACGATAGCC 2298
QY 4082 GGGCTGCTCTGCTTTCAGTTCATTCAGGGCAACCGGACAGGTCCGCTTGACAAAAAGA 4141
    |||
Db 2299 GGGCTGCTCTGCTTTCAGTTCATTCAGGGCAACCGGACAGGTCCGCTTGACAAAAAGA 2358
QY 4142 CCGGGGCGCCCTGCGCTGACGCGGAAACAGCGCGCATCAGAGCAGCCGATTTGCTGT 4201
    |||
Db 2359 CCGGGGCGCCCTGCGCTGACGCGGAAACAGCGCGCATCAGAGCAGCCGATTTGCTGT 2418
QY 4202 GTGCCAGTCATAGCCGAATAGCTCTCAACCCAGCGGCGGAGAACTGCGTGCATC 4261
    |||
Db 2419 GTGCCAGTCATAGCCGAATAGCTCTCAACCCAGCGGCGGAGAACTGCGTGCATC 2478
QY 4262 CATCTGTTCAATCAGCGAAAGATCCTCATCTCTGCTTGAAGAGCTTGAAGTCCCG 4321
    |||
Db 2479 CATCTGTTCAATCAGCGAAAGATCCTCATCTCTGCTTGAAGAGCTTGAAGTCCCG 2538
QY 4322 TCGCCCATCAG 4332
    |||
Db 2539 TCGCCCATCAG 2549
    |||

RESULT 14
US-10-764-818A-19
; Sequence 19, Application US/10764818A
; Publication No. US20040204358A1
; GENERAL INFORMATION:
; APPLICANT: ADVISYS
; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASING CUL
; FILE OF INVENTION: HERD ANIMALS
; FILE REFERENCE: 108328.00170 - AVS1-0033
; CURRENT APPLICATION NUMBER: US/10/764,818A
; CURRENT FILING DATE: 2004-01-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 2716

```

```

; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Codon optimized ("GHRH") sequence for bovine.
US-10-764-818A-19
Query Match 33.6%; Score 1456.2; DB 7; Length 2716;
Best Local Similarity 88.9%; Pred. No. 9.9e-198;
Matches 1663; Conservative 0; Mismatches 28; Indels 180; Gaps 1;

QY 2462 AGAGCGGTTTGGCTATTTGGCGCTCTTCCTGCTTCTGCTCACTGACTCGTGGCTCG 2521
    |||
Db 854 AGTAGGGTTAATTTTCAGCTTGGCTTCCGCTTCTGCTCACTGACTCGTGGCTCG 913
QY 2522 GTTCGTTGGCTGGCGGCGGATACACTCACTCAAGGGGTTAATGAGTTATCCACA 2581
    |||
Db 914 GTTCGTTGGCTGGCGGCGGATACACTCACTCAAGGGGTTAATGAGTTATCCACA 973
QY 2582 GAATCAGGGGATTAACGAGAAAGAAACATGTAGCAAAAGGCCAGCAAAAGGCCAGAAC 2641
    |||
Db 974 GAATCAGGGGATTAACGAGAAAGAAACATGTAGCAAAAGGCCAGCAAAAGGCCAGAAC 1033
QY 2642 CGTAAAGAGCGCGCTTCTGCTGCTTTCATAGAGTCCGCCCTGACGAGCATCAC 2701
    |||
Db 1034 CGTAAAGAGCGCGCTTCTGCTGCTTTCATAGAGTCCGCCCTGACGAGCATCAC 1093
QY 2702 AAAAATCGACCTCAAGTCAAGAGTGGGAAACCCGACAGATTAATGAATACAGGGG 2761
    |||
Db 1094 AAAAATCGACCTCAAGTCAAGAGTGGGAAACCCGACAGATTAATGAATACAGGGG 1153
QY 2762 TTTCCCGTGAAGCTCCCTGCTGCTCTCTGTTCCGACCCCTGACCGATAC 2821
    |||
Db 1154 TTTCCCGTGAAGCTCCCTGCTGCTCTCTGTTCCGACCCCTGACCGATAC 1213
QY 2822 CTGTCGCTTCTTCCTTCGGAAGAGTGGGCTTTCTCAATGCTCACTGTAAGTAT 2881
    |||
Db 1214 CTGTCGCTTCTTCCTTCGGAAGAGTGGGCTTTCTCAATGCTCACTGTAAGTAT 1273
QY 2882 CTCAAGTTGGTGAAGTGGTTCGTCGAAGCTGGGCTGTGTGCAAGAACCCCGCTCAG 2941
    |||
Db 1274 CTCAAGTTGGTGAAGTGGTTCGTCGAAGCTGGGCTGTGTGCAAGAACCCCGCTCAG 1333
QY 2942 CCCGACCGCTGCGCTTATCCGTAACATCTCTTGAAGTCCACCCGTAAGACAGAC 3001
    |||
Db 1334 CCCGACCGCTGCGCTTATCCGTAACATCTCTTGAAGTCCACCCGTAAGACAGAC 1393
QY 3002 TTATGCGCATGCGACAGCCCATCTGTAAACAGAGTTAGCAGAGGATATAGCGGT 3061
    |||
Db 1394 TTATGCGCATGCGACAGCCCATCTGTAAACAGAGTTAGCAGAGGATATAGCGGT 1453
QY 3062 GCTACAGAGTTCTTAAGTGGTGGCTTAATAGGCTTACATAGAGGACAGTATTTGGT 3121
    |||
Db 1454 GCTACAGAGTTCTTAAGTGGTGGCTTAATAGGCTTACATAGAGGACAGTATTTGGT 1513
QY 3122 ATCTGCGCTCTGCTGAAGCAGTTACCTTCGAAAAAGATTGATCTTGAATCCGCG 3181
    |||
Db 1514 ATCTGCGCTCTGCTGAAGCAGTTACCTTCGAAAAAGATTGATCTTGAATCCGCG 1573
QY 3182 AAAACAACACCGCTGTGATGCGGTGTTTTTTTGTGCAACAGATTAACGGCAGA 3241
    |||
Db 1574 AAAACAACACCGCTGTGATGCGGTGTTTTTTTGTGCAACAGATTAACGGCAGA 1633
QY 3242 AAAAAAGATCTCAAGAGATCTTGTATCTTTCTACGGGGTCTGACGCTAGTGAAC 3301
    |||
Db 1634 AAAAAAGATCTCAAGAGATCTTGTATCTTTCTACGGGGTCTGACGCTAG----- 1687
QY 3302 GAAAATCACTTAAGGAGTTTGTGTCATAGCGGATACATATTTGAATGATTTAGAAA 3361
    |||
Db 1688 ----- 1687
QY 3362 AATTAACAAATAGGGGTTCCGGGACATTTCCCGAAAAAGTGCACCTGTATGGGTG 3421
    |||
Db 1688 ----- 1687

```


Search completed: March 15, 2006, 23:47:20
Job time : 1215 secs

Oy	3302	GAAAACTCAGTTAAGGAAATTTGGTATGAGCGGATACATATTTGAATGTATTGTAGAA	3361
Db	1688	-----	1687
Oy	3362	AATAAACAATAAGGGTTTCGGCGACATTTCCCGAAAGTGCCACTGTATCGGGTGTG	3421
Db	1688	-----	1687
Oy	3422	AAATATCCGCACAGATGGGTATAGAGAAATATCCGCATCAGAAATGTAAAGCTTAATA	3481
Db	1688	-----CTAGCG	1693
Oy	3482	TTTCAGAAAGACTCGTCAAGAAAGCGATAGAAAGCGATGCGCTGCGAATCGGAGCGCGCA	3541
Db	1694	CTCAGAAAGAACTTGCTCAAGAAAGCGATAGAAAGCGATGCGCTGCGAATCGGAGCGCGCA	1753
Oy	3542	TACCGTAAAGCAGAGGAAGCGGTCAAGCCCATTTGGCGCCCAAGTCTTTGACAAATATCAC	3601
Db	1754	TACCGTAAAGCAGAGGAAGCGGTCAAGCCCATTTGGCGCCCAAGTCTTTGACAAATATCAC	1813
Oy	3602	GGGTAGCCAAAGCATATGCTCTGTATAGCGGATCCGCAACCCAGCCGCGCAACAGTCATGA	3661
Db	1814	GGGTAGCCAAAGCATATGCTCTGTATAGCGGATCCGCAACCCAGCCGCGCAACAGTCATGA	1873
Oy	3662	ATTCAGAAAAGCGGCATTTTCCACCATGATATTTCCGCAAGCAGGCATTCGCATGGTCA	3721
Db	1874	ATTCAGAAAAGCGGCATTTTCCACCATGATATTTCCGCAAGCAGGCATTCGCATGAGTCA	1933
Oy	3722	CGACGAGATCTTCGCGCGTGGGCAATGCTCGGCTTGAAGCTGGGAGACAGTTCCGCTGGCG	3781
Db	1934	CGACGAGATCTTCGCGCGTGGGCAATGCTCGGCTTGAAGCTGGGAGACAGTTCCGCTGGCG	1993
Oy	3782	CGAGCCCTGATGCTCTTCTGTCAGATCATCTGATCGACAAGACCGGCTTCCATCCGAG	3841
Db	1994	CGAGCCCTGATGCTCTTCTGTCAGATCATCTGATCGACAAGACCGGCTTCCATCCGAG	2053
Oy	3842	TACGTGCTCGCTCGATGCGATGTTTCGTTGGTGTGCAATGGCGAGGTAGCCGGATCA	3901
Db	2054	TACGTGCTCGCTCGATGCGATGTTTCGTTGGTGTGCAATGGCGAGGTAGCCGGATCA	2113
Oy	3902	GGGATATGACGCGCGGCAATTGCATCAGCGATGATGATGATATTTCTCGGACAGACAAAGT	3961
Db	2114	GGGATATGACGCGCGGCAATTGCATCAGCGATGATGATGATATTTCTCGGACAGACAAAGT	2173
Oy	3962	GAGATGACGAGAGATCTCTCCCGGCACTTGCGCCCAATAGACGCCAGTCTCCCTCCGCTT	4021
Db	2174	GAGATGACGAGAGATCTCTCCCGGCACTTGCGCCCAATAGACGCCAGTCTCCCTCCGCTT	2233
Oy	4022	CAGTACAAACGTGACGACAGTGGGCAAGAACCCCGTGTGGCGGCAACGATAGCC	4081
Db	2234	CAGTACAAACGTGACGACAGTGGGCAAGAACCCCGTGTGGCGGCAACGATAGCC	2293
Oy	4082	GCGCTGCTCGTCTTGACATTCATTCAAGGACACCGACAGGTGCTCTTGACAAAAAGAA	4141
Db	2294	GCGCTGCTCGTCTTGACATTCATTCAAGGACACCGACAGGTGCTCTTGACAAAAAGAA	2353
Oy	4142	CCGGGCGCCCTCTGCGCTGACAGCCGGAACACGGCCGCAATCAGAGCAGCCGATTTGTCTTT	4201
Db	2354	CCGGGCGCCCTCTGCGCTGACAGCCGGAACACGGCCGCAATCAGAGCAGCCGATTTGTCTTT	2413
Oy	4202	GGGCCAAGTACAGCGGAATAGCCTCTCCACCCCAAGCGGCGGGAACCTGCGTCAATC	4261
Db	2414	GGGCCAAGTACAGCGGAATAGCCTCTCTCCACCCCAAGCGGCGGGAACCTGCGTCAATC	2473
Oy	4262	CATCTTGTCATTCATGCGAAACGATCCTCATCTGCTCTTGTATCAGAGCTTGATCCC	4321
Db	2474	CATCTTGTCATTCATGCGAAACGATCCTCATCTGCTCTTGTATCAGATCTTGATCCCC	2533
Oy	4322	TGCGGCATCAG 4332	
Db	2534	TGCGGCATCAG 2544	